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Best Local Similarity 100.0%; Pred. No. 0;
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XX	ABU60513;		
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XX	01-MAY-2003	(first entry)	
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XX	Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;		
KW	diagnostic; therapeutic; gene therapy.		
XX	Homo sapiens.		
OS	US2002160384-A1.		
PN	31-OCT-2002.		
XX	14-NOV-2001; 2001US-00925598.		
PF	16-JUN-1997; 97US-0049787P.		
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PR	16-DEC-1999; 99WO-US028634.		
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PR	22-FEB-2000; 2000WO-US004414.		
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PR	24-FEB-2000; 2000WO-US005004.		
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PR	10-MAR-2000; 2000WO-US006319.		
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PR	28-FEB-2001; 2001WO-US006520.		
PR	01-JUN-2001; 2001WO-US017800.		
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PR	29-JUN-2001; 2001WO-US021066.		
PR	03-JUL-2001; 2001WO-US021735.		
PR	28-AUG-2001; 2001US-00941992.		
XX	(GETH) GENENTECH INC.		
XX	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
XX	Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;		
PI	Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;		
PI	Roy MA, Stewart RA, Tamas D, Watanabe CK, Williams PM, Wood WI;		
PI	Zhang Z;		
XX	WPI; 2003-288106/28.		
DR	N-PSDB; ABX90204.		
XX	New transmembrane polypeptides and nucleic acids encoding the		
PT	polypeptides, useful in gene therapy, in chromosome identification, as		
PT	chromosome markers, or in generating probes.		
XX	Claim 12; Fig 95; 650pp; English.		
PS			

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 409 AA;

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 19
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AC ABU96195;
XX
DT 25-JUL-2003 (first entry)
XX
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XX
KW Human; secreted and transmembrane protein; PRO; transgenic animal;
KW knockout; chromosome identification; tissue typing; tumour;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumor necrosis factor-alpha release stimulator.
XX
OS Homo sapiens.
XX
EN US2003036144-A1.
XX

PD
XX
PF 01-JUL-2002; 2002US-00187601.
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PR 18-SEP-1997; 97US-0053263P.
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DT 17-AUG-2003 (first entry)
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
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KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		
KW	tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;		
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XX	PF 25-JUN-2002; 2002US-00180545.		
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PR 30-SEP-1998; 98US-0102487P.
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PR 25-SEP-1998; 98US-0101786P.
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PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
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PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
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PR 06-OCT-1998; 98US-0103258P.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEGEVKGAKNSITDSQMDDEVVYITD 60
QY 61 IQYIPCYQLFSPYNSGGEVNEQALKKILSNVKNVGVWGYKFRHSQDQIMTFRERLLHN 120
Db 61 IQYIPCYQLFSPYNSGGEVNEQALKKILSNVKNVGVWGYKFRHSQDQIMTFRERLLHN 120
QY 121 LQEHFQNQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLQMSQOLGYK 180
Db 121 LQEHFQNQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLQMSQOLGYK 180
QY 181 TVSGSCMSTGFRSAVQTHSSKFFEDGSLKEVHKINEMYASIQEELKICKVEDEQAV 240
Db 181 TVSGSCMSTGFRSAVQTHSSKFFEDGSLKEVHKINEMYASIQEELKICKVEDEQAV 240
QY 241 DKLVDVNRKREIEKRGCAIQAREKNIQKDPENIFLCOALRTPFPNSEFLHSCVMS 300
Db 241 DKLVDVNRKREIEKRGCAIQAREKNIQKDPENIFLCOALRTPFPNSEFLHSCVMS 300
QY 301 LKNRHSVSKSSCNYNHLDVVDNLTLVHTDIPEASPASTPQIIKHKALDLDLRWQFKRS 360
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DT 10-SEP-2003 (first entry)
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003040056-A1.
XX
PD 27-FEB-2003.
XX
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PF 21-JUN-2002; 2002US-00176916.
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PR	29-SEP-1998;	98US-0102331P.	PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.	PR	30-SEP-1998;	98US-0102487P.
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Qy	61	IQKYIPCYQLFSFYNSGSGVNEQALKTLNVKKNVGVGWYKFRHSDQIMTFRERLLHKN	120
Db	61	IQKYIPCYQLFSFYNSGSGVNEQALKTLNVKKNVGVGWYKFRHSDQIMTFRERLLHKN	120
Qy	121	LOEHESNQDLVFLLTPTPIITESCSTHRLSHLYKPKQGLFHRVPLVVAANLGMSEQLGYK	180
Db	121	LOEHESNQDLVFLLTPTPIITESCSTHRLSHLYKPKQGLFHRVPLVVAANLGMSEQLGYK	180
Qy	181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIQBELKSIKCKVEDSQAQV	240
Db	181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIQBELKSIKCKVEDSQAQV	240
Qy	241	DKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS	300
Db	241	DKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS	300
Qy	301	LKNRVKSSCCNNHLDVNDLTLWVHTDIPASPASTPQIIKHKALDLDLDRWQFKRS	360
Db	301	LKNRVKSSCCNNHLDVNDLTLWVHTDIPASPASTPQIIKHKALDLDLDRWQFKRS	360
Qy	361	RLLDQDKRSKANTGSSNQDKASKVSSPETDEIEKMKGFGYRSPTTF	409
Db	361	RLLDQDKRSKANTGSSNQDKASKVSSPETDEIEKMKGFGYRSPTTF	409

RESULT 24
ABR94671
ID ABR94671 standard; protein; 409 AA.
XX
AC ABR94671;
XX
DT 13-SEP-2003 (first entry)

XX	Human secreted polypeptide PRO1013, SEQ ID NO:134.
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XX	Human; PRO; secreted protein; transmembrane protein; TNF-alpha;
KW	extracellular domain; tumour necrosis factor-alpha; cartilage disorder;
KW	chondrocyte; proliferation; differentiation; cancer; tumour; diagnosis;
KW	bone disorder; arthritis; sports injury; cancer; tumour; rectum; cervix;
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW	liver; drug screening; transgenic animal; genetic analysis;
KW	antiarthritic; vulnery; gene therapy.
XX	Homo sapiens.
OS	Homo sapiens.
XX	US2003044926-A1.
PN	06-MAR-2003.
XX	26-JUN-2002; 2002US-00183015.
PD	18-SEP-1997; 97US-0059263P.
XX	18-SEP-1997; 97US-0059263P.
PR	17-OCT-1997; 97US-0062250P.
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PR	07-MAY-1998; 98US-0084639P.
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RESULT 24
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ID ABR94671 standard; protein; 409 AA.
XX
AC ABR94671;
XX
DT 13-SEP-2003 (first entry)

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PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
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PR 17-JUN-1998; 98US-0089538P.
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PR 18-JUN-1998; 98US-0089908P.
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PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
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PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
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PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 15-SEP-1998; 98US-0099812P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100649P.
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PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 25-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-010207P.
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PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLGSGFVLGALAFQHLNLTDSITGEGLLGEVKEAKNSITDSQMDDEVEVYITID 60
DB 1 MEGESTSAVLGSGFVLGALAFQHLNLTDSITGEGLLGEVKEAKNSITDSQMDDEVEVYITID 60
QY 61 IQKYIPCYOLFSPYNSGSEVNEQALKKILSNVKNVGVGYKFRHSDQIMTFRELLHKN 120
DB 61 IQKYIPCYOLFSPYNSGSEVNEQALKKILSNVKNVGVGYKFRHSDQIMTFRELLHKN 120
QY 121 LOEHFSNQDLVFLLLTPSITITSCSTHRLHSLYKPKGLFHRVPLVNVANLQMSQLGYK 180
DB 121 LOEHFSNQDLVFLLLTPSITITSCSTHRLHSLYKPKGLFHRVPLVNVANLQMSQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIQEELKSTCKKVEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIQEELKSTCKKVEDSEQAV 240
QY 241 DKLVKDVNRLKKEIEKRGAQIQAREKNIQKDPQENIFLCOALRTFFPNSFLHSCVMS 300
DB 241 DKLVKDVNRLKKEIEKRGAQIQAREKNIQKDPQENIFLCOALRTFFPNSFLHSCVMS 300
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QY 301 LKRRHVSXSCNHNHLDVVDNLTLMVEHTDIEASGASTPQIIKHKALDLDLRWQFKES 360
Db 301 LKRRHVSXSCNHNHLDVVDNLTLMVEHTDIEASGASTPQIIKHKALDLDLRWQFKES 360
QY 361 RLDDTQKRKANTGSGNQKASKMSSPETDDEIEKMKGGEYSRSTPF 409
Db 361 RLDDTQKRKANTGSGNQKASKMSSPETDDEIEKMKGGEYSRSTPF 409

RESULT 25
ABU13895
ID ABU13895 standard; protein; 409 AA.
XX AC ABU13895;
XX DT 26-FEB-2003 (first entry)
XX DE Human PRO1013 polypeptide.
XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW genetic disorder; antibacterial; immunosuppressive.
XX Homo sapiens.
XX OS US2002103125-A1.
XX EN 01-AUG-2002.
XX PD 20-NOV-2001; 2001US-00989731.
XX PF 16-JUN-1997; 97US-0049787P.
XX PR 17-OCT-1997; 97US-0082250P.
PR 05-NOV-1997; 97WO-US020069P.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
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PR 03-JUN-1998; 98US-0087759P.
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PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
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PR 04-JUN-1998; 98US-0088030P.
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PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.

PR 17-JUN-1998; 98US-0089538P.
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PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
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PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 03-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH LTD.
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;
WPI; 2003-102117/09.
N-PSDB; ABX64050.
Novel secreted and transmembrane polypeptide for modulating biological
activity of cell expressing the polypeptide, identifying agonists or
antagonists of polypeptide, and as molecular weight markers.
Claim 12; Fig 95; 649pp; English.
The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking

CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The polynucleotide sequences
 CC encoding PRO polypeptides are useful as hybridisation probes, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC in the preparation of PRO polypeptides, for generating transgenic animals
 CC or knockout animals, to construct hybridisation probes for mapping the
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome markers, and for generating probes for PCR,
 CC Northern analysis, Southern analysis and Western analysis. ABU13860-
 CC ABU14006 represent the human PRO polypeptides of the invention. Note: The
 CC sequence data for this patent was obtained in electronic format directly
 CC from the USPTO web site at seqdata.uspto.gov/paipedEntry.html
 XX
 SQ Sequence 409 AA;

Query Match 100.0%; Score 409; DB 6; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MEGESTSAVLGFLGALAFQHLNTDSTGELLGKVKGEAKNSITDSQMDVVEVYITD 60

QY 61 IQKIYPCYOLFSGFYNSGSEVNEQALKKILSNVKNVGVGKFRHSDQIMTFRRLHLKN 120
 DB 61 IQKIYPCYOLFSGFYNSGSEVNEQALKKILSNVKNVGVGKFRHSDQIMTFRRLHLKN 120

QY 121 LQEHFSNQDLVLLITPSIITSCSTHRLHSYKPGKGLHRVPLVNVANLGMSEQLGYK 180
 DB 121 LQEHFSNQDLVLLITPSIITSCSTHRLHSYKPGKGLHRVPLVNVANLGMSEQLGYK 180

QY 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASIQEELKICKVEDSEQAV 240
 DB 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASIQEELKICKVEDSEQAV 240

QY 241 DKLVQDVNKLKREIEKRRGAQIQAAAREKNIQKDPQENIFLQALRTPFPNSEFLHSCVMS 300
 DB 241 DKLVQDVNKLKREIEKRRGAQIQAAAREKNIQKDPQENIFLQALRTPFPNSEFLHSCVMS 300

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 DB 301 LKNRVKSSKSCNNHLDVVDNLTLVHTDIPKASPTQIIKHKALDLDLRWQFKRS 360

QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSPTF 409
 DB 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSPTF 409

RESULT 26
 ABU85644
 ID ABU85644 standard; protein; 409 AA.

XX AC ABU85644;

XX DT 02-JUL-2003 (first entry)

XX DE Human PRO polypeptide #67.

XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide;

XX KW tumour necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour;

XX KW cytostatic.

XX OS Homo sapiens.

XX PN US2003036140-A1.

XX PD 20-FEB-2003.

XX PF 01-JUL-2002; 2002US-00187589.

XX PR 26-JUN-1998; 98US-00105413.

PR 16-SEP-1998; 98WO-US019330.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98WO-US021141.
 PR 06-NOV-1998; 98US-00187368.
 PR 01-DEC-1998; 98WO-US025108.
 PR 07-DEC-1998; 98US-00202054.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 25-AUG-1999; 99US-00380137.
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 PR 25-AUG-1999; 99US-00380142.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
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 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 24-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 13-MAR-2000; 2000WO-US008884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941992.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-332028/31.
 N-PSDB; ACA72837.

XX

PT Three hundred and five nucleic acids encoding PRO polypeptides, useful
PT for the manufacture of a medicament for diagnosing or treating tumor.
XX
XX
PS Claim 11; Fig 134; 707pp; English.
XX
XX The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The invention also relates to a method for stimulating the release of
CC tumour necrosis factor alpha (TNF-alpha) from human blood by contacting
CC the blood with a sequence of the invention, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide and a method for detecting the presence of a
CC tumour in a mammal. The polypeptides and polynucleotides are useful for
CC the manufacture of a medicament for diagnosing or treating a tumour in a
CC mammal. Sequences ABU85578-ABU85882 represent human PRO polypeptides of
CC the invention. Note: The sequence data for this patent is also available
CC in electronic format from USPTO at seqdata.uspto.gov/sequence.html
XX
XX Sequence 409 AA;
SQ

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGGFVLGALAQHLNTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
Db 1 MEGESTSAVLGGFVLGALAQHLNTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60

QY 61 IQKIPCYQLFSFYNSGVEVNEQALKILSNKKNVGVWYKPRHSDQIMTFRELLHKN 120
Db 61 IQKIPCYQLFSFYNSGVEVNEQALKILSNKKNVGVWYKPRHSDQIMTFRELLHKN 120

QY 121 LOEHFNSQDLVFLLLTPIITSCSTHRLSHLSYKPKGLFHRVPLVLANGLMSQLGVK 180
Db 121 LOEHFNSQDLVFLLLTPIITSCSTHRLSHLSYKPKGLFHRVPLVLANGLMSQLGVK 180

QY 181 TVSGSCMSTGFSRAVQTHSKFPEEDGSLKEVHKINEMVASYLQELKSIKKVDESEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSKFPEEDGSLKEVHKINEMVASYLQELKSIKKVDESEQAV 240

QY 241 DKLVKDVNRLKRETEKRGQAIOAAREKNIQKDPQENIFLCQALRTFFNFSEFLSCVMS 300
Db 241 DKLVKDVNRLKRETEKRGQAIOAAREKNIQKDPQENIFLCQALRTFFNFSEFLSCVMS 300

QY 301 LKXNHVSKSCNHNHLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDLDRQFKRS 360
Db 301 LKXNHVSKSCNHNHLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDLDRQFKRS 360

QY 361 RLLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSPTF 409
Db 361 RLLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSPTF 409

RESULT 27
ABU98804
ID ABU98804 standard; protein; 409 AA.
XX
XX AC ABU98804;
XX
XX DI 01-AUG-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein PRO1013.
XX
XX KW Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
KW chondrocyte stimulator; tumour; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; TNF-alpha release;
KW tumour necrosis factor alpha release; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; pharmaceutical; diagnostic; biosensor;
bioreactor.
XX
XX OS Homo sapiens.
XX

PN US2003013153-A1.
XX
PD 16-JAN-2003.
XX
PF 19-JUN-2002; 2002US-00175737.
XX
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062280P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
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PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
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PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069135P.
PR 12-DEC-1997; 97US-0069425P.
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PR	25-JUN-1998;	98US-0090576P.	PR	25-SEP-1998;	98US-0102333P.
PR	25-JUN-1998;	98US-0090678P.	PR	30-SEP-1998;	98US-0102487P.
PR	25-JUN-1998;	98US-0090688P.	PR	30-SEP-1998;	98US-0102570P.
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PR	18-AUG-1998;	98US-0096949P.			
PR	18-AUG-1998;	98US-0096959P.			
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PR	01-SEP-1998;	98US-0098716P.			
PR	01-SEP-1998;	98US-0098723P.			
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PR	02-SEP-1998;	98US-0098821P.			

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDDEVVYTID	60
Db	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDDEVVYTID	60
QY	61	IQKIYPCYQLSFYNSGCVNEQALKILSNVKNVGVYKFRHSDQIMTFRERLLHKN	120
Db	61	IQKIYPCYQLSFYNSGCVNEQALKILSNVKNVGVYKFRHSDQIMTFRERLLHKN	120
QY	121	LOEHFNSQDLVFLLLTPSIITESCSTRLEHSLYKPKQGLFHRVPLVAVNLGMSEQLGYK	180
Db	121	LOEHFNSQDLVFLLLTPSIITESCSTRLEHSLYKPKQGLFHRVPLVAVNLGMSEQLGYK	180
QY	181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLOELKSI CKKVEDSQAV	240
Db	181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLOELKSI CKKVEDSQAV	240
QY	241	DKLVKDVNRLKREIEKRGAGIQAAREKNIQKOPQENIFLCQALRTFFPNSEFLHSCVMS	300
Db	241	DKLVKDVNRLKREIEKRGAGIQAAREKNIQKOPQENIFLCQALRTFFPNSEFLHSCVMS	300
QY	301	LKNRHVSKSCNHNHLDVNDNLTMVEHTDIPASASTPQIIKHKALDIDRQWPKRS	360
Db	301	LKNRHVSKSCNHNHLDVNDNLTMVEHTDIPASASTPQIIKHKALDIDRQWPKRS	360
QY	361	RLLDQDKRSKANTGSSNQDKASQVSPETDEEIEKMGKGEYSRSTFF	409
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RESULT 28
ABU98019
ID ABU98019 standard; protein; 409 AA.

XX AC ABU98019;
XX DT 30-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1013.
XX KW Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
KW chondrocyte stimulator; tumour; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome identification.
XX OS Homo sapiens.
XX PN US2003017544-A1.
XX PD 23-JAN-2003.
XX DF 21-JUN-2002; 2002US-00176915.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
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PR	18-AUG-1998;	98US-0096949P.	Db	241	DKLVQVNR	LKRIEIKRGAQIQAAEKNIQKPOENIFLCQALRTFPNSEFLHSCVMS	300
PR	18-AUG-1998;	98US-0096959P.	QY	301	LKNRHVSK	SCNHNHLDVVVDNLTLMVEHTDIPASGASTPQIKKALDLDLDRWQPKRS	360
PR	18-AUG-1998;	98US-0097022P.	Db	301	LKNRHVSK	SCNHNHLDVVVDNLTLMVEHTDIPASGASTPQIKKALDLDLDRWQPKRS	360
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PR	26-AUG-1998;	98US-0097971P.					
PR	26-AUG-1998;	98US-0097974P.					
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PR	25-SEP-1998;	98US-0102240P.					
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PR	30-SEP-1998;	98US-0102487P.					
PR	30-SEP-1998;	98US-0102570P.					
PR	30-SEP-1998;	98US-0102571P.					
PR	01-OCT-1998;	98US-0102684P.					
PR	01-OCT-1998;	98US-0102687P.					
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Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
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Db	1	MEGESTAVLSGFGVLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSOMDDVEVYITD	60				
QY	61	IQYIPCYQLFSFYNSGGEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFERLLHKN	120				
Db	61	IQYIPCYQLFSFYNSGGEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFERLLHKN	120				
QY	121	LOEHFNSQDVLVFLLLTPSIITSCSTRLEHSLYKPKQGLFHRVPLVANLGMSEOLGYK	180				
Db	121	LOEHFNSQDVLVFLLLTPSIITSCSTRLEHSLYKPKQGLFHRVPLVANLGMSEOLGYK	180				
QY	181	TVSGSCNSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQEEELKSIKCKVEDSEQAV	240				
Db	181	TVSGSCNSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASYLQEEELKSIKCKVEDSEQAV	240				

RESULT 29
ABU91725
ID ABU91725 standard; protein; 409 AA.
AC ABU91725;
XX
DT 11-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1013.
XX
KW Human; gene therapy; chromosome identification; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003027277-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176985.
XX
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					Pred. No. 0;

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KW	tumour necrosis factor-alpha; proliferation; differentiation;		
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DB 61 IQKIYPCYQLFSGFYNSGGEVNEQALKILSNVKNVGVYKFRHSQDQIMTFRERLLHKN 120
QY 121 LQEHFSDQDLVLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVAVNLGSEOLGYK 180
DB 121 LQEHFSDQDLVLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVAVNLGSEOLGYK 180
QY 181 TVSGSCMSTGFRSAVQTHSSKFEEDGSLKEVHKINEMYASIQEELKSIKKVEDSEQAV 240
DB 181 TVSGSCMSTGFRSAVQTHSSKFEEDGSLKEVHKINEMYASIQEELKSIKKVEDSEQAV 240
QY 241 DKLVDNRLKREIEYKRGAGQOAAEKNIQKDPQENIFLQALRTFFPNSFLHSCVMS 300
DB 241 DKLVDNRLKREIEYKRGAGQOAAEKNIQKDPQENIFLQALRTFFPNSFLHSCVMS 300
QY 301 LKNRHYSKSSCNYNHLDVVDNLTLVHTDIPEASPASTPQIIKHKALDLDLDRWQFKS 360
DB 301 LKNRHYSKSSCNYNHLDVVDNLTLVHTDIPEASPASTPQIIKHKALDLDLDRWQFKS 360
QY 361 RLLEDQDKRSKANTGSSNQDKASKMSPETDEIEKMGKGFGEYSRPTF 409
DB 361 RLLEDQDKRSKANTGSSNQDKASKMSPETDEIEKMGKGFGEYSRPTF 409

RESULT 31
ABU86259
ID ABU86259 standard; protein; 409 AA.
XX
AC ABU86259;
XX
DT 01-JUL-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) #67.

XX
KW Human; immunogen; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.

OS Homo sapiens.

XX US2003036146-A1.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-00187603.

XX 26-JUN-1998; 98US-00105413.

PR 16-SEP-1998; 98US-0019330.

PR 07-OCT-1998; 98US-00168978.

PR	07-OCT-1998;	98WO-US021141.	PT	the presence of tumor in a mammal.
PR	06-NOV-1998;	98US-00187368.	XX	Claim 11; Fig 134; 707pp; English.
PR	01-DEC-1998;	98WO-US025108.	PS	
PR	07-DEC-1998;	98US-00202054.	XX	
PR	03-MAR-1999;	99US-00254311.	CC	The invention relates to three hundred and five nucleic acids encoding
PR	08-MAR-1999;	99WO-US005028.	CC	PRO polypeptides (secreted and transmembrane), sequences 80% identical to
PR	14-MAY-1999;	99US-00311832.	CC	them, or encoding a PRO polypeptide lacking its associated signal peptide
PR	14-MAY-1999;	99WO-US010733.	CC	or an extracellular domain of the PRO polypeptide, with or lacking its
PR	02-JUN-1999;	99WO-US012252.	CC	associated signal peptide. Also included are the encoded PRO proteins,
PR	25-AUG-1999;	99US-00380137.	CC	PRO expression vectors, host cells transformed with the vector (used to
PR	25-AUG-1999;	99US-00380138.	CC	produce PRO proteins), a chimaeric molecule comprising the PRO
PR	25-AUG-1999;	99US-00380139.	CC	polypeptide fused to a heterologous amino acid sequence, an anti-PRO
PR	25-AUG-1999;	99US-00380142.	CC	antibody, a method for stimulating the release of tumor necrosis factor
PR	01-SEP-1999;	99WO-US020111.	CC	alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
PR	15-SEP-1999;	99WO-US021090.	CC	PRO4337, PRO791, PRO1131, PRO1183, PRO1343, PRO1760, PRO1567 or
PR	18-OCT-1999;	99US-00403297.	CC	PRO4333), a method for stimulating the proliferation or differentiation
PR	12-NOV-1999;	99US-00423844.	CC	of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
PR	01-DEC-1999;	99WO-US028301.	CC	a method for detecting the presence of tumour in a mammal and an
PR	02-DEC-1999;	99WO-US028551.	CC	oligonucleotide probe derived from any of the nucleotide sequences cited
PR	30-DEC-1999;	99WO-US031274.	CC	above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
PR	05-JAN-2000;	2000WO-US000219.	CC	medicament for treating a condition that is responsive to the PRO
PR	18-FEB-2000;	2000WO-US004341.	CC	polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
PR	18-FEB-2000;	2000WO-US004342.	CC	as hybridisation probes in chromosome and gene mapping, or in generating
PR	22-FEB-2000;	2000WO-US004414.	CC	antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
PR	24-FEB-2000;	2000WO-US005044.	CC	polypeptides, in assays to identify other proteins or molecules involved
PR	01-MAR-2000;	2000WO-US005601.	CC	in a binding reaction, to generate transgenic animals or knockout
PR	02-MAR-2000;	2000WO-US005841.	CC	animals, which in turn are useful in the development and screening of
PR	15-MAR-2000;	2000WO-US006884.	CC	therapeutically useful reagents, for chromosome identification, and
PR	30-MAR-2000;	2000WO-US008439.	CC	tissue typing. The PRO polypeptides and nucleic acid molecules are also
PR	17-MAY-2000;	2000WO-US013705.	CC	useful for detecting the presence of a tumour in a mammal, stimulating the
PR	22-MAY-2000;	2000WO-US014042.	CC	proliferation or differentiation of chondrocyte cells, stimulating the
PR	30-MAY-2000;	2000WO-US014941.	CC	release of tumour necrosis factor-alpha from human blood, in gene
PR	02-JUN-2000;	2000WO-US015264.	CC	therapy, or as molecular weight markers for protein electrophoresis
PR	28-JUL-2000;	2000WO-US020710.	CC	purposes. The anti-PRO antibodies may be used in diagnostic assays for
PR	22-AUG-2000;	2000US-00644848.	CC	PRO, or for the affinity purification of PRO from recombinant cell
PR	18-SEP-2000;	2000US-0064610.	CC	culture or natural sources. The present sequence represents a PRO protein
PR	18-SEP-2000;	2000US-00653150.	XX	Sequence 409 AA;
PR	08-NOV-2000;	2000US-00705238.	SQ	
PR	08-NOV-2000;	2000WO-US030952.		Query Match 100.0%; Score 409; DB 6; Length 409;
PR	01-DEC-2000;	2000WO-US032678.		Best Local Similarity 100.0%; Pred. No. 0;
PR	20-DEC-2000;	2000US-00747259.		Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	28-DEC-2000;	2000WO-US034956.	Qy	1 MEGESTSAVLGFLGALAPQHNLNTSDTGEFLGVEKGNKSIITDSQMDVVEVYITD 60
PR	28-FEB-2001;	2001WO-US006520.	Db	1 MEGESTSAVLGFLGALAPQHNLNTSDTGEFLGVEKGNKSIITDSQMDVVEVYITD 60
PR	22-MAR-2001;	2001US-00816744.	Qy	61 IQYIPCYQLFSFYNSSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN 120
PR	10-MAY-2001;	2001US-00854208.	Db	61 IQYIPCYQLFSFYNSSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN 120
PR	25-MAY-2001;	2001US-00854280.	Qy	121 LQEHFSNQDLVFLLLTPTSIITSCSTRHLSLYKPKGLFHRVPLVLANLGMSEQLGYK 180
PR	01-JUN-2001;	2001WO-US017800.	Db	121 LQEHFSNQDLVFLLLTPTSIITSCSTRHLSLYKPKGLFHRVPLVLANLGMSEQLGYK 180
PR	05-JUN-2001;	2001US-00874503.	Qy	181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMVASLOELKSICKKVEDSEQAV 240
PR	20-JUN-2001;	2001WO-US019692.	Db	181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMVASLOELKSICKKVEDSEQAV 240
PR	29-JUL-2001;	2001WO-US021066.	Qy	241 DKLVKNRLKREIEKRGAGIQAAAREKNIQKDPQENIFLCQALRFFPNSEFLHSCVMS 300
PR	09-JUL-2001;	2001US-00917335.	Db	241 DKLVKNRLKREIEKRGAGIQAAAREKNIQKDPQENIFLCQALRFFPNSEFLHSCVMS 300
PR	18-JUL-2001;	2001US-00908827.	Qy	301 LKNRHSVSKSCNHNHLDVVDNLTLMVEHTDIPASPASTPQIKHKALDLDORWQFKRS 360
PR	30-JUL-2001;	2001US-00918585.	Db	301 LKNRHSVSKSCNHNHLDVVDNLTLMVEHTDIPASPASTPQIKHKALDLDORWQFKRS 360
PR	06-AUG-2001;	2001US-00924419.	Qy	361 RLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSPTF 409
PR	13-AUG-2001;	2001US-00929404.	Db	361 RLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSPTF 409
PR	16-AUG-2001;	2001US-00931836.	Qy	
PR	28-AUG-2001;	2001US-00941992.	Db	
PR	29-AUG-2001;	2001WO-US027099.	Qy	
PR	04-SEP-2001;	2001US-00946374.	Db	
PR	15-JAN-2002;	2002US-00052586.	Qy	
XX			Db	
PA	(GETH) GENENTECH INC.			
XX				
PI	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;			
PI	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;			
XX				
DR	WPI; 2003-332034/31.			
DR	N-PSDB; ACA73451.			
XX				
XX	Three hundred and five nucleic acids encoding PRO polypeptides, useful in			
PT	gene therapy, chromosome identification, tissue typing, and for detecting			

ABU67472
 ID ABU67472 standard; protein; 409 AA.
 AC ABU67472;
 DT 29-MAY-2003 (first entry)
 DE Human secreted/transmembrane protein (PRO) #67.
 KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing.
 OS Homo sapiens.
 XX
 XX US2003036162-A1.
 XX
 PD 20-FEB-2003.
 XX
 XX 12-JUL-2002; 2002US-00194423.
 XX
 PR 26-JUN-1998; 98US-00105413.
 PR 16-SEP-1998; 98WO-US019330.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98WO-US021141.
 PR 06-NOV-1998; 98US-00187368.
 PR 01-DEC-1998; 98WO-US025108.
 PR 07-DEC-1998; 98US-00202054.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005801.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.

05-JUN-2001; 2001US-00874503.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 18-JUL-2001; 2001US-00908827.
 30-JUL-2001; 2001US-00918585.
 06-AUG-2001; 2001US-00924419.
 13-AUG-2001; 2001US-00929404.
 16-AUG-2001; 2001US-00931836.
 28-AUG-2001; 2001US-00941992.
 29-AUG-2001; 2001WO-US027099.
 04-SEP-2001; 2001US-00946374.
 15-JAN-2002; 2002US-00052586.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 PI WPI; 2003-332039/31.
 XX DR N-PSDB; ACA05766.
 DR
 DR
 XX
 XX
 PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
 PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
 PT in tissue typing, and in chromosome identification.
 XX
 PS Claim 11; Fig 134; 706pp; English.
 XX
 PS The invention discloses human nucleic acids encoding secreted and
 CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
 CC specifically binds to the PRO polypeptide, a method for stimulating the
 CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
 CC contacting the blood a PRO polypeptide, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells by contacting the
 CC cells with a PRO polypeptide, a method for detecting the presence of a
 CC tumour in a mammal and an oligonucleotide probe derived from any of the
 CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
 CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
 CC preparing PRO polypeptides by recombinant techniques and in gene therapy
 CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
 CC as molecular weight markers for protein electrophoresis purposes, for
 CC chromosome identification, as chromosome markers, as therapeutic agents,
 CC for stimulating the release of TNF-alpha from human blood, for
 CC stimulating the proliferation or differentiation of chondrocytes and
 CC detecting the presence of a tumour. The PRO polypeptides and nucleic
 CC acids may also be used diagnostically for tissue typing. The sequences
 CC presented in ABU67406-ABU67710 are the PRO polypeptides of the invention
 XX
 XX Sequence 409 AA;
 SQ

Query Match 100.0%; Score 409; DB 6; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTGTGFLGKGVKGAQKNSITDSQMDVVEVVTID 60
 |||||
 DB 1 MEGESTSAVLGSGFVLGALAFQHLNLTSDTGTGFLGKGVKGAQKNSITDSQMDVVEVVTID 60
 |||||

QY 61 IQKIYPCYQLSFYNSGSEVNEQALKILSNVKNVGVGWYKFRHSDQINTFPERLLHKN 120
 |||||
 DB 61 IQKIYPCYQLSFYNSGSEVNEQALKILSNVKNVGVGWYKFRHSDQINTFPERLLHKN 120
 |||||

QY 121 LQEHFSNQDLVFLLLTPTSIITSCSTHRLSHSLYKPKQGLFHVPLVWNLGMSQGLGYK 180
 |||||
 DB 121 LQEHFSNQDLVFLLLTPTSIITSCSTHRLSHSLYKPKQGLFHVPLVWNLGMSQGLGYK 180
 |||||

QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLOEELKSIKCKVEDSEQAV 240
 |||||
 DB 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLOEELKSIKCKVEDSEQAV 240
 |||||

QY 241 DKLVKDVNRLKREIKRGAGQIQOAREKNTQKDPQENIFLCQALRTFFNFSEFLHSCVMS 300
 |||||
 DB 241 DKLVKDVNRLKREIKRGAGQIQOAREKNTQKDPQENIFLCQALRTFFNFSEFLHSCVMS 300
 |||||

QY 301 LKNEHVSKSSNNHHLDVNDLTLVVEHTDIDPASPASTPQIKKALDLDNRQFKRS 360
 Db 301 LKNEHVSKSSNNHHLDVNDLTLVVEHTDIDPASPASTPQIKKALDLDNRQFKRS 360
 QY 361 RLDTQDKRSKANTSSNQDKASKMSSPETDEBIEKMKGFGEYSRSPTF 409
 Db 361 RLDTQDKRSKANTSSNQDKASKMSSPETDEBIEKMKGFGEYSRSPTF 409

RESULT 33
 ABU80500
 ID ABU80500 standard; protein; 409 AA.
 XX AC
 XX ABU80500;
 XX 23-JUN-2003 (first entry)
 XX Human PRO protein #67.
 XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
 KW liver; PRO; gene therapy.
 XX Homo sapiens.
 OS
 XX US2003036137-A1.
 XX PD 20-FEB-2003.
 XX PF 27-JUN-2002; 2002US-00184640.
 XX PR 26-JUN-1998; 98US-00105413.
 PR 16-SEP-1998; 98WO-US019330.
 PR 07-OCT-1998; 98US-00169878.
 PR 07-OCT-1998; 98WO-US021141.
 PR 06-NOV-1998; 98US-00181368.
 PR 01-DEC-1998; 98WO-US025108.
 PR 07-DEC-1998; 98US-00202054.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 02-JUN-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380139.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005601.
 PR 15-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US009439.
 PR 22-MAY-2000; 2000WO-US013705.
 PR 30-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US014941.
 PR 28-JUL-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000US-00644848.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941799.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PU, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-342038/32.
 DR N-PSDB; ACA66600.
 XX Three hundred and five nucleic acids encoding secreted and transmembrane
 PRO polypeptides, useful for the diagnosis, prevention and/or treatment
 of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
 cervical or liver tumors.
 XX Claim 11; Fig 134; 708pp; English.
 PS The invention relates to three hundred and five nucleic acids encoding
 CC PRO polypeptides (secreted and transmembrane). Methods and compositions
 CC of the present invention are useful for the diagnosis, prevention and/or
 CC treatment of tumors, such as adrenal, lung, colon, breast, prostate,
 CC rectal, cervical or liver tumors. The PRO polypeptides are also useful
 CC as molecular weight markers, or for chromosome identification. The PRO
 CC genes are useful as hybridisation probes, or for screening libraries of
 CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
 CC therapy, particularly for replacing a defective gene. The present
 CC sequence represents a human PRO polypeptide of the invention
 XX Sequence 409 AA;
 SQ

Query Match 100.0%; Score 409; DB 6; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGESTSAVLGSGVLGALAFQHLNTDSTEGFLGKVGKAKNSITDSQDDVWVYTD 60
 Db 1 MEGESTSAVLGSGVLGALAFQHLNTDSTEGFLGKVGKAKNSITDSQDDVWVYTD 60
 Qy 61 IQKIYPCYQLFSFYNSGGEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFRERLLHN 120
 Db 61 IQKIYPCYQLFSFYNSGGEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFRERLLHN 120
 Qy 121 LOEHFSNODLVFLTLTPSIITTESCSHRLHSLYKPKQGLPHRYPVLVAVNLGMSQGLYK 180
 Db 121 LOEHFSNODLVFLTLTPSIITTESCSHRLHSLYKPKQGLPHRYPVLVAVNLGMSQGLYK 180
 Qy 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLOBELKSI CKKVEDSQAV 240
 Db 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLOBELKSI CKKVEDSQAV 240
 Qy 241 DKLAVKDVNRLKEIEKRGAGIQAAREKNIQDPENIFLQALRTFFPNSFLHSCVMS 300

XX PS Claim 12; Fig 95; 663pp; English.

XX CC The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 203135, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's disease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

XX SQ Sequence 409 AA;

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGFGVLGALAFQHLNLTSDTEGFLGVEGKAKNSITDSQMDVVEVYITD 60
DB 1 MEGESTSAVLGFGVLGALAFQHLNLTSDTEGFLGVEGKAKNSITDSQMDVVEVYITD 60

QY 61 IQKIYPCYQLFSGFYNSGVEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFRERLLHN 120
DB 61 IQKIYPCYQLFSGFYNSGVEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFRERLLHN 120

QY 121 LOEHFNSQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
DB 121 LOEHFNSQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180

QY 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASIQEELKSIKKVEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASIQEELKSIKKVEDSEQAV 240

QY 241 DKLVKDVNRLKREIEKRRGAQIQAREKNIQKDPQENIFLQALRFFPNSEFLHSCVMS 300
DB 241 DKLVKDVNRLKREIEKRRGAQIQAREKNIQKDPQENIFLQALRFFPNSEFLHSCVMS 300

QY 301 LKRRHVSXSSCNYNHLLDVVDNLTLVVEHTDIPEASPASTPQIIKKKALDLDLRWQFKRS 360
DB 301 LKRRHVSXSSCNYNHLLDVVDNLTLVVEHTDIPEASPASTPQIIKKKALDLDLRWQFKRS 360

QY 361 RLDDTDQKRSKANTGSSNQDKASKVSSPETDEIEKMGFGFYSRSPTF 409
DB 361 RLDDTDQKRSKANTGSSNQDKASKVSSPETDEIEKMGFGFYSRSPTF 409

RESULT 35
ABU090886 ID ABU090886 standard; protein; 409 AA.
XX AC AC
XX ABU090886;
XX 11-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1013.
XX KW Human; secreted and transmembrane protein; PRO; antibody therapy;
XX XW pharmaceutical; diagnostic; biosensor; bioreactor.
XX OS Homo sapiens.
XX PN US2003018173-A1.

XX PD 23-JAN-2003.

XX PF 01-MAY-2002; 2002US-00063515.

XX PR 06-DEC-2001; 2001US-00006867.

XX PA (GETH) GENENTECH INC.

XX PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-401702/38.
XX N-PSDB; ACA91174.

XX PT New antibody useful for identifying PRO polypeptides, for affinity
XX purification of PRO polypeptides, and for preparing a medicament for
XX diagnosing or treating conditions responsive to the antibody or PRO
XX polypeptide.

XX PS Disclosure; Fig 22; 345pp; English.

XX CC The invention describes an antibody that specifically binds to a PRO
XX polypeptide having a fully defined amino acid sequence given in the
XX specification. The antibody is useful in identifying PRO polypeptides
XX useful for various industrial applications, including pharmaceuticals,
XX diagnostics, biosensors and bioreactors. The antibody is also used for
XX affinity purification of PRO polypeptides from recombinant cell culture
XX or natural sources. The antibody, PRO polypeptide, or its agonists or
XX antagonists, may be used for preparing a medicament for diagnosing or
XX treating a condition responsive to the antibody, PRO polypeptide, or its
XX agonists or antagonists. This is the amino acid sequence of a novel human
XX secreted and transmembrane PRO polypeptide

XX SQ Sequence 409 AA;

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGFGVLGALAFQHLNLTSDTEGFLGVEGKAKNSITDSQMDVVEVYITD 60
DB 1 MEGESTSAVLGFGVLGALAFQHLNLTSDTEGFLGVEGKAKNSITDSQMDVVEVYITD 60

QY 61 IQKIYPCYQLFSGFYNSGVEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFRERLLHN 120
DB 61 IQKIYPCYQLFSGFYNSGVEVNEQALKILSNVKNVGVGWYKFRHSDQIMTFRERLLHN 120

QY 121 LOEHFNSQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
DB 121 LOEHFNSQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180

QY 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASIQEELKSIKKVEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASIQEELKSIKKVEDSEQAV 240

QY 241 DKLVKDVNRLKREIEKRRGAQIQAREKNIQKDPQENIFLQALRFFPNSEFLHSCVMS 300
DB 241 DKLVKDVNRLKREIEKRRGAQIQAREKNIQKDPQENIFLQALRFFPNSEFLHSCVMS 300

QY 301 LKRRHVSXSSCNYNHLLDVVDNLTLVVEHTDIPEASPASTPQIIKKKALDLDLRWQFKRS 360
DB 301 LKRRHVSXSSCNYNHLLDVVDNLTLVVEHTDIPEASPASTPQIIKKKALDLDLRWQFKRS 360

QY 361 RLDDTDQKRSKANTGSSNQDKASKVSSPETDEIEKMGFGFYSRSPTF 409
DB 361 RLDDTDQKRSKANTGSSNQDKASKVSSPETDEIEKMGFGFYSRSPTF 409

RESULT 36
ABO33945 ID ABO33945 standard; protein; 409 AA.
XX

AC ABO33945;
XX DT 18-SEP-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO1013.
XX KW Human; secreted/transmembrane protein; PRO; tumour; cancer; cytostatic.
XX OS Homo sapiens.
XX PN US2003009013-A1.
XX PD
XX PF 09-JAN-2003.
XX PF 01-MAY-2002; 2002US-00063519.
XX PR 30-DEC-1998; 99KR-000562142.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 14-MAY-1999; 99US-00311832.
XX PR 14-MAY-1999; 99WO-US010753.
XX PR 25-AUG-1999; 99US-00380137.
XX PR 25-AUG-1999; 99US-00380138.
XX PR 25-AUG-1999; 99US-00380139.
XX PR 25-AUG-1999; 99US-00380142.
XX PR 15-SEP-1999; 99US-00397342.
XX PR 18-OCT-1999; 99US-00403297.
XX PR 12-NOV-1999; 99US-00423844.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 02-MAR-2000; 2000WO-US005841.
XX PR 21-MAR-2000; 2000WO-US007532.
XX PR 22-MAY-2000; 2000WO-US014042.
XX PR 02-JUN-2000; 2000WO-US015264.
XX PR 22-AUG-2000; 2000US-00644848.
XX PR 24-AUG-2000; 2000WO-US023328.
XX PR 18-SEP-2000; 2000US-00664610.
XX PR 18-SEP-2000; 2000US-00665350.
XX PR 08-NOV-2000; 2000US-00709238.
XX PR 10-NOV-2000; 2000WO-US030873.
XX PR 01-DEC-2000; 2000WO-US032678.
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XX PR 20-DEC-2000; 2000WO-US034356.
XX PR 28-FEB-2001; 2001WO-US006520.
XX PR 22-MAR-2001; 2001US-00816744.
XX PR 10-MAY-2001; 2001US-00854208.
XX PR 10-MAY-2001; 2001US-00854280.
XX PR 30-MAY-2001; 2001US-00870574.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 05-JUN-2001; 2001US-00874503.
XX PR 29-JUN-2001; 2001US-00869599.
XX PR 18-JUL-2001; 2001US-00908827.
XX PR 06-DEC-2001; 2001US-00006867.
XX PA (GETH) GENENTECH INC.
XX PI Eaton DL, Filvaroff E, Gertzstein ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX PI
XX DR WPI: 2003-447384/42.
XX DR N-FSDB: ACD81551.
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful for
XX the preparation of a medicament for treating disorders with the aberrant
XX expression or activity of the PRO polypeptide, such as tumor conditions
XX and cancer.
XX
XX Disclosure; Fig 22; 223pp; English.
XX
XX The invention relates to an antibody that binds to a secreted or
XX transmembrane protein designated PRO1446 appearing as ABO33941. The
XX protein is one of 84 PRO polypeptides which (along with their encoding
XX nucleic acids) are disclosed in the specification. The methods and

CC compositions of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The antibodies may be used in various
CC diagnostic, competitive binding and/or immunoprecipitation assays. The
CC present sequence represents a PRO polypeptide
XX
XX Sequence 409 AA;
SQ
Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLSCFVLGALAFQHLNTSDTEGELLGKVGKAKNSITDSQMDDEVVYITD 60
DB 1 MEGESTSAVLSCFVLGALAFQHLNTSDTEGELLGKVGKAKNSITDSQMDDEVVYITD 60
QY 61 IQYIICYQLFSPYNSGSEVNEQALKKILSNVKNVGVWGYKFRHSDQIMTFRRLHKN 120
DB 61 IQYIICYQLFSPYNSGSEVNEQALKKILSNVKNVGVWGYKFRHSDQIMTFRRLHKN 120
QY 121 LQEHFSDQDLVLLTTPSIITSCSTHRLHSLYKPKGLFHRVPLVNVANLGMSEQLGYK 180
DB 121 LQEHFSDQDLVLLTTPSIITSCSTHRLHSLYKPKGLFHRVPLVNVANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFRAVQTHSSKFFEDGSLKEVHKINEMYASLQELKSIKCKVEDSEQAV 240
DB 181 TVSGSCMSTGFRAVQTHSSKFFEDGSLKEVHKINEMYASLQELKSIKCKVEDSEQAV 240
QY 241 DKLVDKVNRLKKEIEKRGCAIQIQAAREKNIQDPENIFLQALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDKVNRLKKEIEKRGCAIQIQAAREKNIQDPENIFLQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRVHVKSSQNYNHHLDVVDNLTLVVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRS 360
DB 301 LKNRVHVKSSQNYNHHLDVVDNLTLVVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRS 360
QY 361 RLDDTDQKSKANTGSSNODKASKMSSPETDEIEKMGFGYERSPTF 409
DB 361 RLDDTDQKSKANTGSSNODKASKMSSPETDEIEKMGFGYERSPTF 409
RESULT 37
ABR99418
ID ABR99418 standard; protein; 409 AA.
XX
XX AC ABR99418;
XX DT 18-SEP-2003 (first entry)
XX DE Human secreted polypeptide PRO1013, SEQ ID NO:134.
XX KW Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnary; gene therapy.
XX OS Homo sapiens.
XX PN US2003040063-A1.
XX PD 27-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183006.
XX PR 18-SEP-1997; 97US-0059263P.


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PR 28-MAY-1998; 98US-0087098P;
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PR 02-JUN-1998; 98US-0087609P;
PR 02-JUN-1998; 98US-0087759P;
PR 03-JUN-1998; 98US-0087827P;
PR 04-JUN-1998; 98US-0088025P;
PR 04-JUN-1998; 98US-0088028P;
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PR 05-JUN-1998; 98US-0088212P;
PR 05-JUN-1998; 98US-0088217P;
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PR 26-AUG-1998; 98US-0097952P;
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PR 01-OCT-1998; 98US-0102684P;
PR 01-OCT-1998; 98US-0102687P;

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEGESTSAVLGSGFVLGALAFQHLNTDSDTEGFLGKGEAKNSITDSQMDDEVVYTTID 60
QY 61 IQKIPCYOLFSPYNSGVEVNEQALKILSNVKNVGVGWYKPRRHSQIMTFPERLLHKN 120
DB 61 IQKIPCYOLFSPYNSGVEVNEQALKILSNVKNVGVGWYKPRRHSQIMTFPERLLHKN 120
QY 121 LOEHFSNQDLVFLLLTSPSIITESCSTRLEHSLYKQKGLFHRVPLVWNLGMSQGLGYK 180
DB 121 LOEHFSNQDLVFLLLTSPSIITESCSTRLEHSLYKQKGLFHRVPLVWNLGMSQGLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMVASLOEBLKSICKKYVEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMVASLOEBLKSICKKYVEDSEQAV 240
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PR 02-JUL-1998; 98US-0091628P.
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PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0093282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
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PR 29-SEP-1998; 98US-0102207P.
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Query Match      100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGGFVLGALAFQHLNNTSDTEGFLLGVEYGEAKNSITDSQMDVVEVYITD 60
DB 1 MEGESTSAVLGGFVLGALAFQHLNNTSDTEGFLLGVEYGEAKNSITDSQMDVVEVYITD 60
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Db 61 IQKIIPCYQLFSFYNSGSEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRRLLHKN 120
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Db 121 LQEHFSNQDLVFLLLTFSIITESCSTRLEHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSKKFEEDGSLKEVHKINEMTASLOEBELKICKVEDEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSKKFEEDGSLKEVHKINEMTASLOEBELKICKVEDEQAV 240
QY 241 DKLVKDVNRLKREIEKRGAQIOAREKNIQKDPQENIFLCOALRTFFPNSSEFLHSCVMS 300
Db 241 DKLVKDVNRLKREIEKRGAQIOAREKNIQKDPQENIFLCOALRTFFPNSSEFLHSCVMS 300
QY 301 LKNRHVSKSCNHNHLDVVDNLTLMVHTDIPASASTPOI IKHKLDDDRWQFKRS 360
Db 301 LKNRHVSKSCNHNHLDVVDNLTLMVHTDIPASASTPOI IKHKLDDDRWQFKRS 360
QY 361 RLILDQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSPTF 409
Db 361 RLILDQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSPTF 409

RESULT 40
ABR92231
ID ABR92231 standard; protein; 409 AA.
XX AC ABR92231;
XX DT 13-SEP-2003 (first entry)
XX DE Human secreted polypeptide PRO1013, SEQ ID NO:134.
XX KW Human; PRO; secreted protein; transmembrane protein; TNF-alpha;
XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX KW chondrocyte; proliferation; differentiation; cartilage disorder;
XX KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX KW liver; drug screening; transgenic animal; genetic analysis;
XX KW antiarthritic; vulnery; gene therapy.
XX OS Homo sapiens.
XX PN US2003036160-A1.
XX PD 20-FEB-2003.
XX PE 02-JUL-2002; 2002US-00188781.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 21-OCT-1997; 97US-0063486P.
XX PR 24-OCT-1997; 97US-0063120P.
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XX PR 10-MAR-1998; 98US-0077450P.
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PR 17-SEP-1998; 98US-0100683P.
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PR 17-SEP-1998; 98US-0100930P.
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PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
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PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
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PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.

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DB 1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLIGEVKGEAKNSITQSDMDDEVVYTIID 60		
QY 61	IQKIIPCYQLFSPFNSGGEVNEQALKKILSNKVNKVVGWYKFRHSDQIMTFRERLIHKN 120		
DB 61	IQKIIPCYQLFSPFNSGGEVNEQALKKILSNKVNKVVGWYKFRHSDQIMTFRERLIHKN 120		
QY 121	LOEHFSNQDLVFLLLTTSITSCSTRLEHSLYKPKQGLFHRVPLVAVNLGMSQQLGYK 180		
DB 121	LOEHFSNQDLVFLLLTTSITSCSTRLEHSLYKPKQGLFHRVPLVAVNLGMSQQLGYK 180		
QY 181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMVYASLOELKSIICKYVEDSQAV 240		
DB 181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMVYASLOELKSIICKYVEDSQAV 240		
QY 241	DKLVKDVNRLKREIEKRGAIQAAEKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300		
DB 241	DKLVKDVNRLKREIEKRGAIQAAEKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300		
QY 301	LKNRHVSKSCSNYHNLVDVNTLTMVHEHTDIPASPASTPQIIKHKALDLDORWQPKRS 360		
DB 301	LKNRHVSKSCSNYHNLVDVNTLTMVHEHTDIPASPASTPQIIKHKALDLDORWQPKRS 360		
QY 361	RLLOTQDKRSKANTGSSNQDKASKWSSPETDDEIEKMGFGEXSRSPTF 409		
DB 361	RLLOTQDKRSKANTGSSNQDKASKWSSPETDDEIEKMGFGEXSRSPTF 409		
RESULT 41			
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ID	ABO18872 standard; protein; 409 AA.		
AC	ABO18872;		
AC	ABO18872;		
DT	30-AUG-2003 (first entry)		
DE	Human secreted/transmembrane protein (PRO) #67.		
DE	Human; secreted and transmembrane protein; PRO; TNF-alpha;		
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		
KW	tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;		
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.		
XX	Homo sapiens.		
XX	US2003044925-A1.		
XX	06-MAR-2003.		
XX	25-JUN-2002; 2002US-00180560.		
XX	18-SEP-1997; 97US-0059263P.		
XX	18-SEP-1997; 97US-0059266P.		
XX	17-OCT-1997; 97US-0063250P.		
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XX	24-OCT-1997; 97US-0063120P.		
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XX	28-OCT-1997; 97US-0063540P.		
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PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090252P.	PR	24-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090254P.	PR	25-SEP-1998;	98US-0101786P.
PR	24-JUN-1998;	98US-0090423P.	PR	25-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090433P.	PR	25-SEP-1998;	98US-0102240P.
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PR	26-AUG-1998;	98US-0097974P.			
PR	26-AUG-1998;	98US-0098014P.			
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PR	02-SEP-1998;	98US-0098843P.			
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PR	15-SEP-1998;	98US-0100388P.			
PR	16-SEP-1998;	98US-0100662P.			
PR	16-SEP-1998;	98US-0100664P.			
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PR	16-SEP-1998;	98US-01019330.			
PR	17-SEP-1998;	98US-0100683P.			
PR	17-SEP-1998;	98US-0100684P.			
PR	17-SEP-1998;	98US-0100919P.			
PR	17-SEP-1998;	98US-0100930P.			

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Best Local Similarity 100.0%; Pred No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
Db 1 MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
Qy 61 IQKIYFCYQLFSPYNSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN 120
Db 61 IQKIYFCYQLFSPYNSGVEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLLHKN 120
Qy 121 LQEHFSDQLVFLLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVAVANLGMSEOLGYK 180
Db 121 LQEHFSDQLVFLLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVAVANLGMSEOLGYK 180
Qy 181 TVSGSCMSTGFSRAVQTHSKFEEGSLKEVHKINEMTASLQELKSI CKKVEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSKFEEGSLKEVHKINEMTASLQELKSI CKKVEDSEQAV 240
Qy 241 DKLVKDVNRLKREIKRGAQIQAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
Db 241 DKLVKDVNRLKREIKRGAQIQAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
Qy 301 LKNRHYKSCSNYHLDVVDNLITLVEHTDIPASASTPQIIKHKALDLDLRWQFKES 360
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Qy 361 RLDDTDKRSKANTGSSNQDKASKMSSPETDEIERKMGFGYRSRPTF 409
Db 361 RLDDTDKRSKANTGSSNQDKASKMSSPETDEIERKMGFGYRSRPTF 409

RESULT 42
ABR78293
ID ABR78293 standard; protein; 409 AA.
XX AC ABR78293;
XX DT 19-SEP-2003 (first entry)
XX DE Human secreted polypeptide PRO1013, SEQ ID NO:134.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;

KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.

OS Homo sapiens.

PN US2003054474-A1.

PN 20-MAR-2003.

XX 22-JUL-2002; 2002US-00201530.

XX 22-JUN-1998; 98US-0090254P.

PR 02-JUN-1998; 98WO-US012252P.

PR 25-AUG-1999; 99US-00380137.

PR 28-FEB-2001; 2001WO-US006520.

PR 15-JAN-2002; 2002US-00052586.

XX (GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-503631/47.

XX N-PSDB; ACP00166.

XX Claim 11; Fig 134; 700pp; English.

CC The invention relates to human PRO secreted/transmembrane polypeptides
CC (ABR78227-ABR78531) and nucleic acids encoding them (ACF00100-00404). The
CC invention also relates to sequences at least 80% identical to the PRO
CC nucleic acid and polypeptide sequences of the invention, recombinant
CC vectors and host cells comprising a PRO nucleic acid, a method for the
CC recombinant production of a PRO polypeptide, antibodies against a PRO
CC polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic
CC acids encoding PRO polypeptides of the invention were initially
CC identified via homology screening using consensus sequences based on the
CC extracellular domain sequences from known secreted proteins. Human cDNA
CC libraries containing sequences of interest were identified using
CC oligonucleotides based on the consensus sequences, and cDNA clones were
CC isolated and characterized. The PRO polypeptides are useful for
CC stimulating release of tumour necrosis factor- α (TNF- α) from
CC human blood and may thus be used in the treatment of conditions in which
CC enhanced TNF- α release would be beneficial. They are also useful for
CC stimulating the proliferation or differentiation of chondrocytes and as
CC such may be used in the treatment of various bone and/or cartilage
CC disorders such as arthritis and sports injuries. The PRO polypeptides may
CC be used in a method for detecting the presence of a tumour (e.g., an
CC adrenal tumour, lung tumour, colon tumour, breast tumour, prostate
CC tumour, rectal tumour, cervical tumour or liver tumour) in a mammal. This
CC method involves comparing the level of expression of the PRO polypeptide
CC polypeptide in the test sample as compared to the control sample is
CC indicative of the presence of a tumour. The PRO polypeptides are
CC additionally useful for in drug screening to identify agonists and
CC antagonists of PRO polypeptides. PRO nucleic acids are useful as
CC hybridisation probes (for isolation of cDNA molecules), in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA and in gene
CC therapy. The nucleic acids can also be used for mapping genes encoding
CC PRO polypeptides, for genetic analysis of individuals with genetic
CC disorders, and for generating either transgenic animals or knock-out
CC animals which are useful in the development and screening of
CC therapeutically useful compounds. Sequences ABR78227-ABR78531 represent
CC the human PRO secreted/transmembrane polypeptides of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPIO at seqdata.uspto.gov/sequence.html

XX Sequence 409 AA;

XX Query Match 100.0%; Score 409; DB 6; Length 409;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLGFLGALAFQHLNTSDTDEGFLLGKVGKAKNSITDSQMDVVEVYITD 60
DB 1 MEGESTSAVLGFLGALAFQHLNTSDTDEGFLLGKVGKAKNSITDSQMDVVEVYITD 60
QY 61 IQYIFCYQLFSFYNSGVEVNEQALKILSNVKNVGVWYKFRHSDQIMTFRILLHKN 120
DB 61 IQYIFCYQLFSFYNSGVEVNEQALKILSNVKNVGVWYKFRHSDQIMTFRILLHKN 120
QY 121 LQHFNSQDLVFLLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVLANLGMSEOLGYK 180
DB 121 LQHFNSQDLVFLLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVLANLGMSEOLGYK 180
QY 181 TVSGCMSTGFSRAVQTHSSKPFEDGSLKEVHKINEMVASIQERLKSICKKVEDSEQAV 240
DB 181 TVSGCMSTGFSRAVQTHSSKPFEDGSLKEVHKINEMVASIQERLKSICKKVEDSEQAV 240
QY 241 DKLVKDVNRLKREIKERGAQIOAAREKNIQKDPQENIFLCOALRTFFPNSSEFLHSCVMS 300
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DB 301 LKNRHVSKSSCNYNHLDVVDNLTLAVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRS 360
QY 361 RLDDTQDKSKANTGSSNQDKASKMSSPETDEIEKMGKGFGEYSRSPTF 409
DB 361 RLDDTQDKSKANTGSSNQDKASKMSSPETDEIEKMGKGFGEYSRSPTF 409

RESULT 43

ABU71962

ID ABU71962 standard; protein; 409 AA.

XX AC ABU71962;

XX DT 11-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO1013.

XX KW Human; secreted and transmembrane polypeptide; chromosome mapping;

XX KW gene mapping; transgenic animal; knockout animal;

XX KW therapeutic agent screening; chromosome identification; tissue typing;

XX KW gene therapy.

XX OS Homo sapiens.

XX PN US2003018183-A1.

XX PD 23-JAN-2003.

XX PF 01-MAY-2002; 2002US-00063512.

XX PR 06-DEC-2001; 2001US-00006867.

XX XX (GETH) GENENTECH INC.

XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX DR WPI; 2003-330984/31.

XX DR N-PSDB; ACR60373.

XX PT New secreted and transmembrane PRO polypeptides and nucleic acid
XX PT molecules encoding the polypeptides, useful in gene therapy or preparing
XX PT a medicament for treating a condition that is responsive to the PRO
XX PT polypeptide or antibody.

XX PS Disclosure; Fig 22; 409pp; English.

XX CC The invention describes novel isolated PRO polypeptides. The PRO

CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 409 AA;

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGFLVLCALAFQHLNTDSTEGFLGCEVKGAKNITDSQMDDEVVYITD 60
Db 1 MEGESTSAVLGFLVLCALAFQHLNTDSTEGFLGCEVKGAKNITDSQMDDEVVYITD 60

QY 61 IQKIYPCYQLFSFYNSGVEVNEQALKILSNVKNVGVGKFRHSDQIMTFRERLLHN 120
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QY 121 LOEHFSNQDLVLLITPSTIITSCSTHRLSHLYKPKQGLFHRVPLVVANLCMSEQLYK 180
Db 121 LOEHFSNQDLVLLITPSTIITSCSTHRLSHLYKPKQGLFHRVPLVVANLCMSEQLYK 180

QY 181 TVSGSCMTGFGRAVQTHSSKFFEDGSLKEVHKINEMVYASIQBELKICKKVEDSEQAV 240
Db 181 TVSGSCMTGFGRAVQTHSSKFFEDGSLKEVHKINEMVYASIQBELKICKKVEDSEQAV 240

QY 241 DKLVKDVNLRKREIEKRGQAQIQAAREKNIQKDPQENIFLQALRTFPNPEFLHSCVMS 300
Db 241 DKLVKDVNLRKREIEKRGQAQIQAAREKNIQKDPQENIFLQALRTFPNPEFLHSCVMS 300

QY 301 LKNRHVSKSSCNVNHLDVVDNLTLVHEHTDIPEASPTPQIIKHKALDLDLRWQFKRS 360
Db 301 LKNRHVSKSSCNVNHLDVVDNLTLVHEHTDIPEASPTPQIIKHKALDLDLRWQFKRS 360

QY 361 RLDDTDKRSKANTGSSNQDKASKMSPTDEIEKMKGFGYSRSPTF 409
Db 361 RLDDTDKRSKANTGSSNQDKASKMSPTDEIEKMKGFGYSRSPTF 409

RESULT 44
ABU85029
ID ABU85029 standard; protein; 409 AA.
XX
AC ABU85029;
XX
DT 30-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1013.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
KW chondrocyte stimulator; chromosome mapping; gene mapping;
KW transgenic animal; knock-out animal; tumour.
XX
OS Homo sapiens.
XX
PN US2003032114-A1.
XX
PD 13-FEB-2003.
XX
PF 20-JUN-2002; 2002US-00176919.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASLOBELKSI CKKYEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASLOBELKSI CKKYEDSEQAV 240
Qy 241 DKLVKDVNRLKREIEKRGAGIQAAREKNIQKDPQENIFLQALRFFPNSEFLHSCVMS 300
Db 241 DKLVKDVNRLKREIEKRGAGIQAAREKNIQKDPQENIFLQALRFFPNSEFLHSCVMS 300
Qy 301 LKRRHVSKSSCNVNHLDVVDNITLVEHTDIPASPASTPQIIKHKALDLDORWQFKRS 360
Db 301 LKRRHVSKSSCNVNHLDVVDNITLVEHTDIPASPASTPQIIKHKALDLDORWQFKRS 360
Qy 361 RLDDTDQKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSTFF 409
Db 361 RLDDTDQKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSTFF 409

RESULT 45
ABO00168
ID ABO00168 standard; protein; 409 AA.
XX
AC ABO00168;
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XX 06-AUG-2003 (first entry)
DT Novel human secreted and transmembrane protein PRO1013.
XX
DE
XX Human; gene therapy; tumour necrosis factor alpha; TNF-alpha;
KW chondrocyte stimulation; tumour; tissue typing.
XX
XX Homo sapiens.
XX
XX US2003032101-A1.
PN
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PD 13-FEB-2003.
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XX 17-JUN-2002; 2002US-00173695.
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XX XX 26-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #67.
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX XX US2003036124-A1.
XX XX 20-FEB-2003.
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS
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XX XX
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Best Local Similarity 100.0%; Pred. No. 0;
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DB 1 MEGESTSAVLGCVLGAFAQHLLNTSDTEGFLGKVGKAKNSITDSQMDDEVVYITD 60
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DB 61 IQKYIPCYOLFSPYNSGGEVNEQALKKILSNVKNVGVWYKFRHSQDQIMTFRELLHKN 120
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DB 121 LOEHFSNQLVFLLLTPSIITSCSTHRLSHSLYKPKGLFHRVPLVYVANTGMSEQLGYK 180
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DB 181 TVSGSCMTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASIQBELKSI CKKVEDSEQAV 240
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AC ABU8719;
DT 09-JUL-2003 (first entry)
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KW chondrocyte proliferation; chondrocyte differentiation; tumour detection;
KW tissue typing.
OS Homo sapiens.
PN US2003036133-A1.
PD 20-FEB-2003.
PF 27-JUN-2002; 2002US-00184630.
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Qy 61 IQKYPICYQLFSFYNSGGEVNEQALKILSNVKKNVGVGWYKFRHSDQIMTFERLLHKN 120
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Qy 121 LOEHESNODLVLTLTPTSIITSCSTHRLBHSYKPKQGLFHVPLVAVNLGSEQLGYK 180
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KW Chondrocyte stimulator; chromosome mapping; gene mapping;
KW transgenic animal; knockout animal; tissue typing;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumour necrosis factor-alpha stimulation; TNF-alpha stimulation.
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PR 01-OCT-1998; 98US-0102687P.
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PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.

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Best Local Similarity 100.0%; Pred. No. 0;
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Db 61 IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVYKPRRHSQDQIMTFRLLHKN 120
Qy 121 LQEHFNSQDLVFLLLTPSIITSCSTRLEHSLYKPKGLPHRVLVWLVANLQMSQOLGYK 180
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RESULT 53
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XX
XX ABO19177;
AC
AC ABO19177;
DT
DT 27-AUG-2003 (first entry)
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XX Novel human secreted and transmembrane protein PRO1013.
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XX Human; secreted and transmembrane protein; PRO; chromosome mapping;
XX gene mapping; transgenic animal; knockout animal; tissue typing;
XX chromosome identification; tumour; chondrocyte proliferation;
XX chondrocyte differentiation; tumour necrosis factor-alpha release;
XX gene therapy.
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XX OS Homo sapiens.
XX PN US2003036118-A1.
XX PD 20-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176760.
XX PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
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PR 18-OCT-1999; 99US-00433297.
PR 12-NOV-1999; 99US-00423844.
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PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
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PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
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PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.

PR 15-JAN-2002; 2002US-00052586.
XX (GETH) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-402071/38.
DR N-PSDB; ACD25424.
XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, chromosome identification, tissue typing, for detecting
PT the presence of tumor in a mammal, or as hybridization probes in gene
PT mapping.
XX Claim 11; SEQ ID NO 134; 707pp; English.
XX The invention describes a novel isolated PRO polypeptide. The PRO
CC polypeptide or anti-PRO antibody is useful for preparing a medicament for
CC treating a condition that is responsive to the PRO polypeptide or anti-
CC PRO antibody. The PRO nucleotide sequences are useful as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful for detecting
CC the presence of tumour in a mammal, stimulating proliferation or
CC differentiation of chondrocyte cells, stimulating the release of tumour
CC necrosis factor-alpha from human blood, in gene therapy, or as molecular
CC weight markers for protein electrophoresis purposes. The anti-PRO
CC antibodies may be used in diagnostic assays for PRO, or for the affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX Sequence 409 AA;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 181 TVSGSCMSTGFSRAVQTHSKPFEDGSLKEVHKINEMVASYLQEBELKSKKVEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSKPFEDGSLKEVHKINEMVASYLQEBELKSKKVEDSEQAV 240
Qy 241 DKLVKDVNRLKREIEKRGAGIQAAREKNIQKDPQNIIFLQALRTFFPNSFLHSCVMS 300
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Qy 301 LKNRHYKSSCNYNHLDVVNLTLMVEHTDIPASPASTPQIHKHALDLDLRWQFKRS 360
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Qy 361 RLDDTDQKRSKANTGSSNQDKASKMSSPETDEIERKMGFGFYSRPTF 409
Db 361 RLDDTDQKRSKANTGSSNQDKASKMSSPETDEIERKMGFGFYSRPTF 409

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XX		98US-0087759P
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KW	tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;	98US-0088028P
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.	98US-0088029P
XX		98US-0088033P
OS	Homo sapiens.	98US-0088326P
XX		98US-0088361P
XX	US2003036123-A1.	98US-0088202P
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PR	23-SEP-1998;	98US-0101477P.					
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KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;		
KW	liver; drug screening; transgenic animal; genetic analysis;		
KW	antiarthritic; vulnery; gene therapy.		
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OS	Homo sapiens.		
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Mismatches

Indels

Gaps

Score

DB

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PR 10-SEP-1998; 98US-0099812P.

CC and cancer. They can also be used to generate transgenic or knockout
 CC animals useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
 CC molecular weight markers for protein electrophoresis, chromosome
 CC identification and tissue typing. The PRO polypeptides are useful to
 CC induce angiogenesis e.g wound healing; in the treatment of sports-related
 CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis; diabetes; hyperinsulinaemia and hypoinulinaemia. The
 CC antibodies may be used in various diagnostic, competitive binding and/or
 CC immunoprecipitation assays. The present sequence represents the amino
 CC acid sequence of a PRO polypeptide of the invention

XX Sequence 409 AA;

Query Match 100.0%; Score 409; DB 6; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGCVLGALAFQHLNLTDSDETEGLGKVGKAKNSITDSQDDVEVYITD 60
 DB 1 MEGESTSAVLGCVLGALAFQHLNLTDSDETEGLGKVGKAKNSITDSQDDVEVYITD 60

QY 61 IQKIYPCVQLFQFYNSSGEVNEQALKKILSNVKNVGVWYKFRHSQDQIMTFRERLLHKN 120
 DB 61 IQKIYPCVQLFQFYNSSGEVNEQALKKILSNVKNVGVWYKFRHSQDQIMTFRERLLHKN 120

QY 121 LOEHFNSQDLVFLLLTPSIITESCSTHRLSHLYKPKQGLFHRVPLVVANLGMSEQLGYK 180
 DB 121 LOEHFNSQDLVFLLLTPSIITESCSTHRLSHLYKPKQGLFHRVPLVVANLGMSEQLGYK 180

QY 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASLOELKSI CKKVEDSQAV 240
 DB 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASLOELKSI CKKVEDSQAV 240

QY 241 DKLVKDVNRLKREIEKRGAQIQARAKNIQKDPQENIFLQALRTFPNSEFLHSCVMS 300
 DB 241 DKLVKDVNRLKREIEKRGAQIQARAKNIQKDPQENIFLQALRTFPNSEFLHSCVMS 300

QY 301 LKNRVKSSCCNYNHLVDVNLTLMVHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
 DB 301 LKNRVKSSCCNYNHLVDVNLTLMVHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360

QY 361 RLDDTQDKRSKANTSSNQDKASKMSPETDEETKMKGFGEYSRSTPF 409
 DB 361 RLDDTQDKRSKANTSSNQDKASKMSPETDEETKMKGFGEYSRSTPF 409

RESULT 59

ID ABU65635

XX ABU65635 standard; protein; 409 AA.

XX AC ABU65635;

XX DT 19-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein, SEQ ID 134.

XX KW Human; PRO; secreted protein; transmembrane protein; cytostatic;
 KW antiarthritic; osteopathic; adrenal tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; cervical tumour;
 KW liver tumour; TNF-alpha release; arthritis; tumour necrosis factor alpha;
 KW chondrocyte cell; bone disorder; cartilage disorder; sports injury.

XX OS Homo sapiens.

XX PN US2003036156-A1.

XX PD 20-FEB-2003.

XX PF 02-JUL-2002; 2002US-00188767.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTDEGFLLGVEKGEAKNSITDSQMDVVEVYITD	60
Qy	61	IQYIPCYQLFSYNSGGEVNEQALKILSNVKNVGVYKFRHSDQIMTFRERLLHKN	120
Db	61	IQYIPCYQLFSYNSGGEVNEQALKILSNVKNVGVYKFRHSDQIMTFRERLLHKN	120
Qy	121	LQEHFSNQDLVFLLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVANLGMSEQLGYK	180
Db	121	LQEHFSNQDLVFLLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVANLGMSEQLGYK	180
Qy	181	TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASLOEELKSICKVEDSEQAV	240
Db	181	TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASLOEELKSICKVEDSEQAV	240
Qy	241	DKLVQVNLKRETEKRGAGIQAAEKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS	300
Db	241	DKLVQVNLKRETEKRGAGIQAAEKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS	300
Qy	301	LKNEHVSCKSNVNHLDVVNDLTLVVEHTDIPEASGASTPQIKKHALDLDWRQPKRS	360
Db	301	LKNEHVSCKSNVNHLDVVNDLTLVVEHTDIPEASGASTPQIKKHALDLDWRQPKRS	360
Qy	361	RLDQTKRSKANTGSSNQDKASKMSSPDETEKMKGFGEYSRSTPF	409
Db	361	RLDQTKRSKANTGSSNQDKASKMSSPDETEKMKGFGEYSRSTPF	409

RESULT 60

ABO07483

ID ABO07483 standard; protein; 409 AA.

XX ABO07483;

XX AC

XX 18-AUG-2003 (first entry)

XX Human PRO polypeptide #67.

DE

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; cytostatic;
KW tumour necrosis factor-alpha; TNF-alpha; blood; tumour; chondrocyte cell;
KW cancer.
XX
OS Homo sapiens.
XX
PN US2003032117-A1.
XX
PD 13-FEB-2003.
XX
PF 24-JUN-2002; 2002US-00179510.
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PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
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PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
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PR 02-JUL-1998; 98US-0091626P.
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PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
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PR 26-AUG-1998; 98US-0097955P.

PR	26-AUG-1998;	98US-0097971P.	Query Match	100.0%;	Score 409;	DB 6;	Length 409;
PR	26-AUG-1998;	98US-0097974P.	Best Local Similarity	100.0%;	Pred. No. 0;		
PR	26-AUG-1998;	98US-0098014P.	Matches 409;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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PR	01-SEP-1998;	98US-0098723P.	1	MEGESTSAVLGSGFLGALAFQHLNTSDTEGFLGKGNKSIITDSQMDVVEVYIID	60		
PR	02-SEP-1998;	98US-0098803P.	61	IQYIPCYQLPSFNSGVEVNEQAKKILSNVKNVGVGWYKPRRHSQDQMTFRERLLHN	120		
PR	02-SEP-1998;	98US-0098821P.	61	IQYIPCYQLPSFNSGVEVNEQAKKILSNVKNVGVGWYKPRRHSQDQMTFRERLLHN	120		
PR	02-SEP-1998;	98US-0098843P.	121	LOEHFSNQDLVFLLLTTSITSCSTRLEHSLYKPKGLFHRVPLVWNLGWSQLGYK	180		
PR	02-SEP-1998;	98US-0098862P.	121	LOEHFSNQDLVFLLLTTSITSCSTRLEHSLYKPKGLFHRVPLVWNLGWSQLGYK	180		
PR	09-SEP-1998;	98US-0099602P.	191	TVSSGCMSTGFSRAVQTHSKPFEEGSLKEVHKINEMVASYLOEELKSI CKKVDESEQAV	240		
PR	10-SEP-1998;	98US-0099741P.	181	TVSSGCMSTGFSRAVQTHSKPFEEGSLKEVHKINEMVASYLOEELKSI CKKVDESEQAV	240		
PR	10-SEP-1998;	98US-0099754P.	241	DKLVKNRLKREIKERGAQIOAAREKNIQKDPQENIFLCOALRFFFNSEFFLHSCVMS	300		
PR	10-SEP-1998;	98US-0099763P.	241	DKLVKNRLKREIKERGAQIOAAREKNIQKDPQENIFLCOALRFFFNSEFFLHSCVMS	300		
PR	15-SEP-1998;	98US-0099812P.					
PR	15-SEP-1998;	98US-0100388P.					
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PR	16-SEP-1998;	98US-0100684P.					
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PR	17-SEP-1998;	98US-0100919P.					
PR	17-SEP-1998;	98US-0100930P.					
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PR	23-SEP-1998;	98US-0101471P.					
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PR	23-SEP-1998;	98US-0101477P.					
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Qy	361	RLLDTDQKRKANTGSSNODKASKSSPETDEIEKMGKGFGEYSRPTF	409
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XX	AC	ABO03670;	
XX	XX	10-AUG-2003 (first entry)	
DE	XX	Human secreted/transmembrane protein (PRO) #67.	
KW	XX	Human; secreted and transmembrane protein; PRO; TNF-alpha;	
KW	XX	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	
KW	XX	tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;	
XX	XX	prostate tumour; rectal tumour; cervical tumour; liver tumour.	
OS	XX	Homo sapiens.	
FN	XX	US2003036128-A1.	
XX	XX	20-FEB-2003.	
XX	XX	27-JUN-2002; 2002US-00184616.	
PR	18-SEP-1997;	97US-0059263P.	
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PR	17-OCT-1997;	97US-0062250P.	
PR	21-OCT-1997;	97US-0063486P.	
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PR	24-OCT-1997;	97US-0063121P.	
PR	28-OCT-1997;	97US-0063540P.	
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PR	28-OCT-1997;	97US-0063544P.	
PR	28-OCT-1997;	97US-0063564P.	
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PR	31-OCT-1997;	97US-0063870P.	
PR	31-OCT-1997;	97US-0064103P.	
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PR	24-NOV-1997;	97US-0066466P.	
PR	24-NOV-1997;	97US-0066772P.	
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PR	17-DEC-1997;	97US-0069870P.	
PR	18-DEC-1997;	97US-0068017P.	
PR	10-MAR-1998;	98US-0077450P.	
PR	11-MAR-1998;	98US-0077632P.	
PR	11-MAR-1998;	98US-0077649P.	
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PR	18-MAY-1998;	98US-0086023P.	PR	18-AUG-1998;	98US-0098959P.
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PR	22-MAY-1998;	98US-0086486P.	PR	26-AUG-1998;	98US-0097952P.
PR	28-MAY-1998;	98US-0087098P.	PR	26-AUG-1998;	98US-0097954P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097955P.
PR	02-JUN-1998;	98US-0087603P.	PR	26-AUG-1998;	98US-0097971P.
PR	02-JUN-1998;	98US-0087753P.	PR	26-AUG-1998;	98US-0097974P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0098014P.
PR	04-JUN-1998;	98US-0088025P.	PR	26-AUG-1998;	98US-0098716P.
PR	04-JUN-1998;	98US-0088028P.	PR	01-SEP-1998;	98US-0098723P.
PR	04-JUN-1998;	98US-0088029P.	PR	01-SEP-1998;	98US-0098803P.
PR	04-JUN-1998;	98US-0088033P.	PR	02-SEP-1998;	98US-0098821P.
PR	04-JUN-1998;	98US-0088325P.	PR	02-SEP-1998;	98US-0098843P.
PR	05-JUN-1998;	98US-0088167P.	PR	03-SEP-1998;	98US-0098602P.
PR	05-JUN-1998;	98US-0088202P.	PR	10-SEP-1998;	98US-0099741P.
PR	05-JUN-1998;	98US-0088212P.	PR	10-SEP-1998;	98US-0099754P.
PR	09-JUN-1998;	98US-0088217P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088655P.	PR	10-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088722P.	PR	15-SEP-1998;	98US-0100388P.
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PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0101751P.
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PR	10-JUN-1998;	98US-0088825P.	PR	17-SEP-1998;	98US-0100683P.
PR	10-JUN-1998;	98US-0088826P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100319P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100330P.
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PR	12-JUN-1998;	98US-0089103P.	PR	18-SEP-1998;	98US-0101068P.
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PR	16-JUN-1998;	98US-0089514P.	PR	23-SEP-1998;	98US-0101472P.
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PR	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101477P.
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PR	19-JUN-1998;	98US-0089952P.	PR	24-SEP-1998;	98US-0101743P.
PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090252P.	PR	25-SEP-1998;	98US-0101786P.
PR	22-JUN-1998;	98US-0090254P.	PR	25-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090429P.	PR	29-SEP-1998;	98US-0102240P.
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PR	24-JUN-1998;	98US-0090461P.	PR	29-SEP-1998;	98US-0102487P.
PR	24-JUN-1998;	98US-0090535P.	PR	30-SEP-1998;	98US-0102570P.
PR	24-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090676P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090678P.	PR	01-OCT-1998;	98US-0102687P.
PR	25-JUN-1998;	98US-0090688P.	PR	02-OCT-1998;	98US-0102965P.
PR	25-JUN-1998;	98US-0090690P.	PR	06-OCT-1998;	98US-0103258P.
PR	25-JUN-1998;	98US-0090694P.	PR	06-OCT-1998;	98US-0103449P.
PR	25-JUN-1998;	98US-0090695P.			
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PR	26-JUN-1998;	98US-0090696P.			
PR	26-JUN-1998;	98US-00105413			
PR	26-JUN-1998;	98US-0090862P.			
PR	26-JUN-1998;	98US-0090863P.			
PR	26-JUN-1998;	98US-0091010P.			
PR	01-JUL-1998;	98US-0091359P.			
PR	01-JUL-1998;	98US-0091544P.			
PR	02-JUL-1998;	98US-0091478P.			
PR	02-JUL-1998;	98US-0091486P.			

Query Match 100.0%; Score 409; DB 6; Length 409;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGKGNKSNITDSQMDDEVVYITID 60

Db 1 MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGKGNKSNITDSQMDDEVVYITID 60

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Db	61	IQKIPYQVLF	SYN	SGEVNEQ	ALKKILSNVKNVGVGMYKFRHSDQIMTFRELLHKV	120	
QY	121	LOEHFSNODLV	FL	LT	SIITESC	THRLHSLYKPKGLFHRVPLVAVNLGMSQOLGYK	180
Db	121	LOEHFSNODLV	FL	LT	SIITESC	THRLHSLYKPKGLFHRVPLVAVNLGMSQOLGYK	180
QY	181	TVSGSCMSTG	FSRAVQ	THSSKFF	EDGSLKEVHKINEMYASLQBELKSI	CKKVEDSEQAV	240
Db	181	TVSGSCMSTG	FSRAVQ	THSSKFF	EDGSLKEVHKINEMYASLQBELKSI	CKKVEDSEQAV	240
QY	241	DKLVKDVNLR	KRETEKRG	AGIQ	IAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS	300	
Db	241	DKLVKDVNLR	KRETEKRG	AGIQ	IAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS	300	
QY	301	LKNEHVSKSS	CNVNHL	VDVNL	TLVMEHTDIP	PEASPASTPQIIKHKALDLDORWQPKRS	360
Db	301	LKNEHVSKSS	CNVNHL	VDVNL	TLVMEHTDIP	PEASPASTPQIIKHKALDLDORWQPKRS	360
QY	361	RLLTQDKRS	KANTGSS	NQDKAS	KMSSPETDEEIEKMGGEYSRSPTF	409	
Db	361	RLLTQDKRS	KANTGSS	NQDKAS	KMSSPETDEEIEKMGGEYSRSPTF	409	
RESULT 62							
ABR67118							
ID	ABR67118 standard; protein; 409 AA.						
XX	AC ABR67118;						
XX	DT 05-AUG-2003 (first entry)						
DE	Human secreted polypeptide PRO1013, SEQ ID NO:134.						
KW	Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnery; gene therapy.						
OS	Homo sapiens.						
XX	US2003027266-A1.						
XX	PD 06-FEB-2003.						
XX	PF 18-JUN-2002; 2002US-00174588.						
XX	18-SEP-1997;	97US-0059263P.					
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PR	04-JUN-1998;	98US-0088025P.				
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PR	04-JUN-1998;	98US-0088326P.				
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PR	05-JUN-1998;	98US-0088202P.				
PR	05-JUN-1998;	98US-0088212P.				
PR	05-JUN-1998;	98US-0088217P.				
PR	03-JUN-1998;	98US-0088555P.				
PR	10-JUN-1998;	98US-0088722P.				
PR	10-JUN-1998;	98US-0088738P.				
PR	10-JUN-1998;	98US-0088740P.				
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PR	10-JUN-1998;	98US-0088825P.				
PR	10-JUN-1998;	98US-0088826P.				
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PR	11-JUN-1998;	98US-0088863P.				
PR	11-JUN-1998;	98US-0088876P.				
PR	12-JUN-1998;	98US-0089090P.				
PR	12-JUN-1998;	98US-0089105P.				
PR	16-JUN-1998;	98US-0089512P.				
PR	16-JUN-1998;	98US-0089514P.				
PR	17-JUN-1998;	98US-0089538P.				
PR	17-JUN-1998;	98US-0089598P.				
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PR	18-JUN-1998;	98US-0089908P.				
PR	19-JUN-1998;	98US-0089952P.				
PR	22-JUN-1998;	98US-0090246P.				
PR	22-JUN-1998;	98US-0090252P.				
PR	22-JUN-1998;	98US-0090254P.				
PR	24-JUN-1998;	98US-0090429P.				

PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102240P.
PR	24-JUN-1998;	98US-0090444P.	PR	29-SEP-1998;	98US-0102330P.
PR	24-JUN-1998;	98US-0090461P.	PR	29-SEP-1998;	98US-0102331P.
PR	24-JUN-1998;	98US-0090535P.	PR	30-SEP-1998;	98US-0102487P.
PR	24-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102570P.
PR	25-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090678P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102687P.
PR	25-JUN-1998;	98US-0090690P.	Query Match 100.0%; Score 409; DB 6; Length 409;		
PR	25-JUN-1998;	98US-0090694P.	Best Local Similarity 100.0%; Pred. No. 0;		
PR	25-JUN-1998;	98US-0090695P.	Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
PR	25-JUN-1998;	98US-0090696P.			
PR	26-JUN-1998;	98US-0010541.3			
PR	26-JUN-1998;	98US-0090862P.	Qy	1	MEGESTAVLSGFGVIGALAFQHLNTSDTEGFLGVEKGEAKNSITDSOMDDVEVVTID 60
PR	26-JUN-1998;	98US-0090863P.	Db	1	MEGESTAVLSGFGVIGALAFQHLNTSDTEGFLGVEKGEAKNSITDSOMDDVEVVTID 60
PR	26-JUN-1998;	98US-0091010P.	Qy	61	IQYIPCYQLFSFYNSSGVEVNEQALKILSNVKNVGVYKFRHSDQIMTFPERLLHKN 120
PR	01-JUL-1998;	98US-0091359P.	Db	61	IQYIPCYQLFSFYNSSGVEVNEQALKILSNVKNVGVYKFRHSDQIMTFPERLLHKN 120
PR	01-JUL-1998;	98US-0091544P.	Qy	121	LOEHFNSQDLVFLLLTPSIITESCSTRHLSLYKPKQGLFHRVPLVANLGMSEQLYK 180
PR	02-JUL-1998;	98US-0091478P.	Db	121	LOEHFNSQDLVFLLLTPSIITESCSTRHLSLYKPKQGLFHRVPLVANLGMSEQLYK 180
PR	02-JUL-1998;	98US-0091486P.	Qy	181	TVSGSCMSTGFSRAVQTHSSKPFEEGSLKEVHKINEMVASLOEELKSI CKVEDSEQAV 240
PR	02-JUL-1998;	98US-0091626P.	Db	181	TVSGSCMSTGFSRAVQTHSSKPFEEGSLKEVHKINEMVASLOEELKSI CKVEDSEQAV 240
PR	02-JUL-1998;	98US-0091628P.	Qy	241	DKLVKQVNRLLKREIKRGAQIOAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
PR	02-JUL-1998;	98US-0091633P.	Db	241	DKLVKQVNRLLKREIKRGAQIOAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
PR	24-JUL-1998;	98US-0094006P.	Qy	301	LKRVHVKSSCNVNHLDVVNDLTLVHEHTDIEASPASTPQIIKHKALDLDORWQFKRS 360
PR	04-AUG-1998;	98US-0095282P.	Db	301	LKRVHVKSSCNVNHLDVVNDLTLVHEHTDIEASPASTPQIIKHKALDLDORWQFKRS 360
PR	10-AUG-1998;	98US-0095998P.	Qy	361	RLLDQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGEYSRPTF 409
PR	10-AUG-1998;	98US-0096012P.	Db	361	RLLDQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGEYSRPTF 409
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PR	17-AUG-1998;	98US-0096766P.	ABO15721		
PR	17-AUG-1998;	98US-0096867P.	ID ABO15721 standard; protein; 409 AA.		
PR	17-AUG-1998;	98US-0096869P.	XX ABO15721;		
PR	17-AUG-1998;	98US-0096897P.	AC ABO15721;		
PR	18-AUG-1998;	98US-0096949P.	XX 27-AUG-2003 (first entry)		
PR	18-AUG-1998;	98US-0096959P.	DT Human secreted/transmembrane protein (PRO) #67.		
PR	26-AUG-1998;	98US-0097022P.	XX Human; secreted and transmembrane protein; PRO; TNF-alpha;		
PR	26-AUG-1998;	98US-0097954P.	DE Human; secreted and transmembrane protein; PRO; TNF-alpha;		
PR	26-AUG-1998;	98US-0097955P.	KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		
PR	26-AUG-1998;	98US-0097971P.	KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;		
PR	26-AUG-1998;	98US-0097974P.	KW prostate tumour; rectal tumour; cervical tumour; liver tumour.		
PR	26-AUG-1998;	98US-0098014P.	XX Homo sapiens.		
PR	01-SEP-1998;	98US-0098716P.	OS Homo sapiens.		
PR	01-SEP-1998;	98US-0098723P.	XX US2003054483-A1.		
PR	02-SEP-1998;	98US-0098803P.	PN 20-MAR-2003.		
PR	02-SEP-1998;	98US-0098821P.	XX 26-JUL-2002; 2002US-00205907.		
PR	02-SEP-1998;	98US-0098843P.	XX 05-JUN-2000; 2000US-0209832P.		
PR	09-SEP-1998;	98US-0099602P.	PR 28-FEB-2001; 2001WO-US006520.		
PR	10-SEP-1998;	98US-0099741P.	PR 15-JAN-2002; 2002US-00052586.		
PR	10-SEP-1998;	98US-0099754P.	XX (GETH) GENENTECH INC.		
PR	10-SEP-1998;	98US-0099763P.	PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;		
PR	10-SEP-1998;	98US-0099812P.	XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;		
PR	15-SEP-1998;	98US-0100388P.			
PR	16-SEP-1998;	98US-0100662P.			
PR	16-SEP-1998;	98US-0100664P.			
PR	16-SEP-1998;	98US-0101751P.			
PR	16-SEP-1998;	98WO-US019330			
PR	17-SEP-1998;	98US-0100683P.			
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PR	17-SEP-1998;	98US-0100919P.			
PR	17-SEP-1998;	98US-0100930P.			
PR	18-SEP-1998;	98US-0100849P.			
PR	18-SEP-1998;	98US-0101014P.			
PR	18-SEP-1998;	98US-0101068P.			
PR	23-SEP-1998;	98US-0101471P.			
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PR	23-SEP-1998;	98US-0101477P.			
PR	24-SEP-1998;	98US-0101738P.			
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PR	24-SEP-1998;	98US-0101743P.			
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PR	25-SEP-1998;	98US-0101786P.			
PR	29-SEP-1998;	98US-0102207P.			

PR	15-MAY-1998;	98US-0085579P.	PR	17-AUG-1998;	98US-0096766P.
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PR	15-MAY-1998;	98US-0085582P.	PR	17-AUG-1998;	98US-0096891P.
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PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0096959P.
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PR	04-JUN-1998;	98US-0088326P.	PR	02-SEP-1998;	98US-0098821P.
PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-0098843P.
PR	05-JUN-1998;	98US-0088202P.	PR	09-SEP-1998;	98US-0099602P.
PR	05-JUN-1998;	98US-0088212P.	PR	10-SEP-1998;	98US-0099741P.
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PR	05-JUN-1998;	98US-0088225P.	PR	10-SEP-1998;	98US-0099763P.
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PR	10-JUN-1998;	98US-0088740P.	PR	15-SEP-1998;	98US-0100388P.
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PR	10-JUN-1998;	98US-0088825P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088826P.	PR	16-SEP-1998;	98WO-US019330.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100683P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100684P.
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PR	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101472P.
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PR	22-JUN-1998;	98US-0090254P.	PR	24-SEP-1998;	98US-0101743P.
PR	24-JUN-1998;	98US-0090429P.	PR	24-SEP-1998;	98US-0101922P.
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PR	24-JUN-1998;	98US-0090444P.	PR	25-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090461P.	PR	29-SEP-1998;	98US-0102240P.
PR	24-JUN-1998;	98US-0090535P.	PR	29-SEP-1998;	98US-0102330P.
PR	24-JUN-1998;	98US-0090540P.	PR	29-SEP-1998;	98US-0102330P.
PR	25-JUN-1998;	98US-0090676P.	PR	29-SEP-1998;	98US-0102331P.
PR	25-JUN-1998;	98US-0090678P.	PR	30-SEP-1998;	98US-0102457P.
PR	25-JUN-1998;	98US-0090688P.	PR	30-SEP-1998;	98US-0102570P.
PR	25-JUN-1998;	98US-0090690P.			
PR	25-JUN-1998;	98US-0090694P.			
PR	25-JUN-1998;	98US-0090695P.			
PR	25-JUN-1998;	98US-0090696P.			
PR	26-JUN-1998;	98US-00105413.			
PR	26-JUN-1998;	98US-0090862P.			
PR	26-JUN-1998;	98US-0090863P.			
PR	26-JUN-1998;	98US-0091010P.			
PR	01-JUL-1998;	98US-0091359P.			
PR	01-JUL-1998;	98US-0091544P.			
PR	02-JUL-1998;	98US-0091478P.			
PR	02-JUL-1998;	98US-0091486P.			
PR	02-JUL-1998;	98US-0091626P.			
PR	02-JUL-1998;	98US-0091628P.			
PR	02-JUL-1998;	98US-0091632P.			
PR	24-JUL-1998;	98US-0094006P.			
PR	04-AUG-1998;	98US-0095282P.			
PR	10-AUG-1998;	98US-0095998P.			
PR	10-AUG-1998;	98US-0096012P.			
PR	17-AUG-1998;	98US-0096757P.			

Query Match

Best Local Similarity

Matches

100.0%;

100.0%;

409;

Score

409;

DB

6;

Length

409;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

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60

Db

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240

QY 241 DKLVDVNLKREIEKRGAGIQAAEKNQKODPOENIFLCOALRTFFPNSFLHSCVMS 300
DB 241 DKLVDVNLKREIEKRGAGIQAAEKNQKODPOENIFLCOALRTFFPNSFLHSCVMS 300
QY 301 LKNRHSVSSCNYNHLDVVDNLTLVVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
DB 301 LKNRHSVSSCNYNHLDVVDNLTLVVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
QY 361 RLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSPTF 409
DB 361 RLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSPTF 409

RESULT 65
ID ABU72297 standard; protein; 409 AA.
XX
AC ABU72297;
DT 16-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #11.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression.
OS Homo sapiens.
XX
FN US2002182638-A1.
XX
PD 05-DEC-2002.
XX
PF 02-MAY-2002; 2002US-00063547.
XX
PR 30-DEC-1998; 98KX-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 15-SEP-1999; 99US-00403297.
PR 12-OCT-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644849.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 30-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX

(GETH) GENENTECH INC.
Eaton DL, Filvaroff B, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI,
XX
XX WPI; 2003-328612/04.
DR N-PSDB; ACA63996.
XX
PT An isolated secreted transmembrane polypeptide designated PRO, useful as
a therapeutic agent.
XX
PS Disclosure; Fig 22; 236pp; English.
XX
The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides and polynucleotides are useful for preparing a medicament
useful in the treatment of a condition responsive to anti-PRO antibody.
Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting
its expression in specific cells, tissues or serum, and for affinity
purification of PRO from recombinant cell culture or natural sources.
CC ABU72287-ABU72370 represent the human PRO polypeptides of the invention
XX
SQ Sequence 409 AA;
Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLGFGVGLGALAFQHLNTDSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
DB 1 MEGESTSAVLGFGVGLGALAFQHLNTDSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
QY 61 IQKIYPCYQLFSPFYNSSGVEVNEQALKILSNKVNKVGHYKFRHSQDQIMTFRLLHKN 120
DB 61 IQKIYPCYQLFSPFYNSSGVEVNEQALKILSNKVNKVGHYKFRHSQDQIMTFRLLHKN 120
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DB 121 LQEHFNSQDLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVAVANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFRSAVQTHSSKFFEDGSLKVEHKINEMVYASIQEELKSTCKKVEDSEQAV 240
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DB 241 DKLVDVNLKREIEKRGAGIQAAEKNQKODPOENIFLCOALRTFFPNSFLHSCVMS 300
QY 301 LKNRHSVSSCNYNHLDVVDNLTLVVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
DB 301 LKNRHSVSSCNYNHLDVVDNLTLVVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
QY 361 RLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSPTF 409
DB 361 RLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSPTF 409

RESULT 66
ABU65330 standard; protein; 409 AA.
XX
AC ABU65330;
DT 16-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #67.
XX
KW Human; PRO; cytostatic; chromosome mapping; gene mapping;
KW protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;
KW chondrocyte differentiation; chondrocyte proliferation; tumour.
XX
OS Homo sapiens.

XX US2003032102-A1.
PN 13-FEB-2003.
XX 17-JUN-2002; 2002US-00173697.
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0082250P.
PR 21-OCT-1997; 97US-0083486P.
PR 24-OCT-1997; 97US-00631120P.
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KW	chromosome mapping; gene mapping; transgenic animal; knock-out animal;
KW	tumour.
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Best Local Similarity 100.0%; Pred. No. 0;
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XX DT 10-JUN-2003 (first entry)
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KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW differentiation; tumour; gene therapy.
XX OS Homo sapiens.
XX PN US2003036143-A1.
XX PD 20-FEB-2003.
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PR	26-AUG-1998	98US-0097974P
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PF	02-JUL-2002; 2002US-00187885.
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15-JAN-2002;	2002US-00052586.

19-AUG-2003 (first entry)

Human secreted polypeptide PRO1013, SEQ ID NO:134.

Human: pp0: secreted protein: transmembrane protein

extracellular domain; tumour necrosis factor- α ; TNF- α ;
chondrocyte; proliferation; differentiation; cartilage disorder.

bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;

adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis;

antiarthritic; vulnerary; gene therapy.

Homo sapiens.

■

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL; Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPT: 2003-341977/32.

New secreted and transmembrane PRO polypeptide useful in preparing a N-PSDB; ACC91060.

Claim 11; Fig 134; 707pp; English.

The invention relates to human PRO secreted/transmembrane polypeptides (ABR69963-ABR70267) and nucleic acids encoding them (ACC90994-ACC91298).

CC The invention also relates to sequences at least 80% identical to the PRO
CC nucleic acid and polypeptide sequences of the invention, recombinant
CC vectors and host cells comprising a PRO nucleic acid, a method for the
CC recombinant production of a PRO polypeptide, antibodies against a PRO
CC polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic
CC acids encoding PRO polypeptides of the invention were initially
CC identified via homology screening using consensus sequences based on the
CC extracellular domain sequences from known secreted proteins. Human cDNA
CC libraries containing sequences of interest were identified using
CC oligonucleotides based on the consensus sequences, and cDNA clones were
CC isolated and characterised. The PRO polypeptides are useful for
CC stimulating release of tumour necrosis factor-alpha (TNF-alpha) from
CC human blood and may thus be used in the treatment of conditions in which
CC enhanced TNF-alpha release would be beneficial. They are also useful for
CC stimulating the proliferation or differentiation of chondrocytes and as
CC such may be used in the treatment of various bone and/or cartilage
CC disorders such as arthritis and sports injuries. The PRO polypeptides may
CC be used in a method for detecting the presence of a tumour (e.g., an
CC adrenal tumour, lung tumour, colon tumour, breast tumour, prostate
CC tumour, rectal tumour, cervical tumour or liver tumour) in a mammal. This
CC method involves comparing the level of expression of the PRO polypeptide
CC in test and control samples, where a higher level of expression of PRO
CC polypeptide in the test sample as compared to the control sample is
CC indicative of the presence of a tumour. The PRO polypeptides are
CC additionally useful for in drug screening to identify agonists and
CC antagonists of PRO polypeptides. PRO nucleic acids are useful as
CC hybridisation probes (for isolation of cDNA molecules), in chromosome and
CC gene mapping. The nucleic acids can also be used for mapping genes encoding
CC therapy. The nucleic acids can also be used for individuals with genetic
CC PRO polypeptides, for genetic analysis of individuals with genetic
CC disorders, and for generating either transgenic animals or knock-out
CC animals which are useful in the development and screening of
CC therapeutically useful compounds. Sequences ABR6993-ABR70267 represent
CC the human PRO secreted/transmembrane polypeptides of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 409 AA;

Query Match		100.0%;	Score 409;	DB 6;	Length 409;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 409;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MEGESTSAVLGFGVLCALAFQHLNDSDETEGFLGVEGKNSITDSQMDVVEVVTID	60		
Db	1	MEGESTSAVLGFGVLCALAFQHLNDSDETEGFLGVEGKNSITDSQMDVVEVVTID	60		
QY	61	IQKYIFCYQLFFPYNSSGEVNEQALKILSNVKNVGVWYKFRHSDQIMTFRELLHKN	120		
Db	61	IQKYIFCYQLFFPYNSSGEVNEQALKILSNVKNVGVWYKFRHSDQIMTFRELLHKN	120		
QY	121	LQEHFSDQLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVWNLGMSQLGYK	180		
Db	121	LQEHFSDQLVFLLLTPSIITSCSTHRLHSLYKPKGLFHRVPLVWNLGMSQLGYK	180		
QY	181	TVSGSCWSTGFSRAVOTHSKPFEDGSLKEVHKINEMVYASLQEBLKSKICKVEDSEQAV	240		
Db	181	TVSGSCWSTGFSRAVOTHSKPFEDGSLKEVHKINEMVYASLQEBLKSKICKVEDSEQAV	240		
QY	241	DKLVKDVNRLKRIEIKRGAQIOAREKNIQKDPQENIFLCOALRTFFPNSFHLSCVMS	300		
Db	241	DKLVKDVNRLKRIEIKRGAQIOAREKNIQKDPQENIFLCOALRTFFPNSFHLSCVMS	300		
QY	301	LKNRHSVSKSCNNHLLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDLRQFKRS	360		
Db	301	LKNRHSVSKSCNNHLLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDLRQFKRS	360		
QY	361	RLDLDQDKRSKANTGSSNQDKASKMSPTDEIEIKMGFGGYSRSPTF	409		
Db	361	RLDLDQDKRSKANTGSSNQDKASKMSPTDEIEIKMGFGGYSRSPTF	409		

RESULT 71

ABR69362	ID	ABR69362 standard; protein; 409 AA.
XX	AC	ABR69362;
XX	DT	11-AUG-2003 (first entry)
XX	DE	Human secreted polypeptide PRO1013, SEQ ID NO:134.
XX	KW	Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnertary; gene therapy.
XX	OS	Homo sapiens.
XX	PN	US2003036132-A1.
XX	PD	20-FEB-2003.
XX	PF	28-JUN-2002; 2002US-00184629.
XX	PR	18-SEP-1997; 97US-0059263P.
XX	PR	18-SEP-1997; 97US-0059266P.
XX	PR	17-OCT-1997; 97US-0062250P.
XX	PR	21-OCT-1997; 97US-0063486P.
XX	PR	24-OCT-1997; 97US-0063120P.
XX	PR	24-OCT-1997; 97US-0063121P.
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AC AB001503;
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DT 07-AUG-2003 (first entry)
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KW Human; PRO; tumour; cytostatic; cancer; secreted protein; lung;
KW transmembrane protein; tumour necrosis factor alpha; TNF-alpha; adrenal;
KW chondrocyte cell; colon; breast; prostate; rectum; cervix; liver.
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OS Homo sapiens.
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PR 09-JUL-2001; 2001WO-US021735.
PR 29-AUG-2001; 2001WO-US027099.
PR 15-JAN-2002; 2002US-00052586.

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(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-341328/32.

N-PSDB; ACD06999.

Three hundred and five nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO, useful for detecting the presence of, or treating tumor, e.g. adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumor.

Claim 11; Fig 134; 707pp; English.

The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody that specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood with a PRO polypeptide and a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO

CC polypeptide. The polypeptides and polynucleotides are useful for
 CC detecting the presence of a tumour, such as an adrenal, lung, colon,
 CC breast, prostate, rectal, cervical or liver tumour, and for treating such
 CC tumours. The polynucleotides are useful as hybridisation probes, in
 CC chromosome and gene mapping and in generating antisense RNA or DNA. The
 CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
 CC bioreactors. Both are useful in tissue typing. Sequences ABO01437-
 CC ABO01741 represent human PRO polypeptides of the invention. Note: The
 CC sequence data for this patent is also available in electronic format from
 CC USPTO at seqdata.uspto.gov/sequence.html
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DB 61	IOKXIPCYOLFQFYNSSGEVNEQALKKILSNVKNVGVWYKPRRSDQIMTFRELLHKN	120		
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DB 181	TVSGSCWSTGFRNAVOTHSKFEEDGSLKEVHKINEMVYASIQEELKSIKCKVEDSEQAV	240		
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XX AC ABU81305;

XX DT 24-JUN-2003 (first entry)

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XX KW Human; PRO; tumour necrosis factor-alpha; TNF-alpha; blood;

XX KW chondrocyte cell; tumour; adrenal; kidney; lung; colon; breast; prostate;

XX KW rectum; cervix; liver; cytostatic.

XX OS Homo sapiens.

XX PN US2003017542-A1.

XX PD 23-JAN-2003.

XX PF 20-JUN-2002; 2002US-00176749.

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DT 28-JUL-2003 (first entry)
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KW Human; PRO; secreted protein; transmembrane protein; TNF-alpha;
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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy.
XX Homo sapiens.
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XX New isolated, secreted and transmembrane PRO polypeptide, useful for the
PT diagnosis, prevention and treatment of rectal, lung, stomach, esophageal
PT or skin cancers.
XX
XX Disclosure; Fig 22; 235pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO polypeptide
CC and polynucleotide sequences are useful for the diagnosis, prevention and
CC treatment of rectal, lung, stomach, esophageal or skin tumors, and/or
CC cancers. The PRO polypeptides are also useful as molecular weight
CC markers. The PRO polynucleotide sequences are useful for chromosome
CC identification, hybridisation probes, and for screening libraries of
CC human cDNA, genomic DNA or mRNA. They may also be used in gene therapy,
CC particularly for replacing a defective gene. ABU90960-ABU91043 represent
CC the human PRO polypeptides of the invention
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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
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KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		
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KW	liver; drug screening; transgenic animal; Genetic analysis;		
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XX			
PD	13-FEB-2003.		
XX			
PF	01-JUL-2002; 2002US-00187594.		
XX			
PR	26-JUN-1998; 98US-00105413.		
PR	15-SEP-1998; 98WO-US019330.		
PR	07-OCT-1998; 98US-00168978.		
PR	06-NOV-1998; 98WO-US021141.		
PR	01-DEC-1998; 98WO-US02108.		
PR	07-DEC-1998; 98US-00202054.		
PR	03-MAR-1999; 99US-00254311.		
PR	08-MAR-1999; 99WO-US008028.		
PR	14-MAY-1999; 99US-00311832.		
PR	02-JUN-1999; 99WO-US010733.		
PR	25-AUG-1999; 99US-00380137.		
PR	25-AUG-1999; 99US-00380138.		
PR	25-AUG-1999; 99US-00380139.		

25-AUG-1999; 99US-00380142.
01-SEP-1999; 99WO-US020111.
15-SEP-1999; 99WO-US021090.
18-OCT-1999; 99US-00403297.
12-NOV-1999; 99US-00423844.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028551.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004414.
22-FEB-2000; 2000WO-US004504.
24-FEB-2000; 2000WO-US005004.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005841.
15-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
22-AUG-2000; 2000US-00644848.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
08-NOV-2000; 2000US-00709238.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
22-MAR-2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00908827.
30-JUL-2001; 2001US-00918585.
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13-AUG-2001; 2001US-00929404.
16-AUG-2001; 2001US-00931836.
28-AUG-2001; 2001US-00941992.
29-AUG-2001; 2001WO-US027099.
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15-JAN-2002; 2002US-00052586.

(GETH) GENENTECH INC.
Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
WPI; 2003-466225/44.
N-ESDB; ACC92902.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful
in gene therapy, or for preparing a medicament for treating a condition
that is responsive to the PRO polypeptide or anti-PRO antibody.
Claim 11; Fig 134; 707pp; English.
The invention relates to human PRO secreted/transmembrane polypeptides
(ABR71793-ABR72097) and nucleic acids encoding them (ACC92836-ACC93140).
The invention also relates to sequences at least 80% identical to the PRO
nucleic acid and polypeptide sequences of the invention, recombinant
vectors and host cells comprising a PRO nucleic acid, a method for the
recombinant production of a PRO polypeptide, antibodies against a PRO
polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic
acids encoding PRO polypeptides of the invention were initially

CC identified via homology screening using consensus sequences based on the
 CC extracellular domain sequences from known secreted proteins. Human cDNA
 CC libraries containing sequences of interest were identified using
 CC oligonucleotides based on the consensus sequences, and cDNA clones were
 CC isolated and characterised. The PRO polypeptides are useful for
 CC stimulating release of tumour necrosis factor-alpha (TNF-alpha) from
 CC human blood and may thus be used in the treatment of conditions in which
 CC enhanced TNF-alpha release would be beneficial. They are also useful for
 CC stimulating the proliferation or differentiation of chondrocytes and as
 CC such may be used in the treatment of various bone and/or cartilage
 CC disorders such as arthritis and sports injuries. The PRO polypeptides may
 CC be used in a method for detecting the presence of a tumour (e.g., an
 CC adrenal tumour, lung tumour, colon tumour, breast tumour, prostate
 CC tumour, rectal tumour, cervical tumour or liver tumour) in a mammal. This
 CC method involves comparing the level of expression of the PRO polypeptide
 CC in test and control samples, where a higher level of expression of PRO
 CC polypeptide in the test sample as compared to the control sample is
 CC indicative of the presence of a tumour. The PRO polypeptides are
 CC additionally useful for in drug screening to identify agonists and
 CC antagonists of PRO polypeptides. PRO nucleic acids are useful as
 CC hybridisation probes (for isolation of cDNA molecules), in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA and in gene
 CC therapy. The nucleic acids can also be used for mapping genes encoding
 CC PRO polypeptides, for genetic analysis of individuals with genetic
 CC disorders, and for generating either transgenic animals or knock-out
 CC animals which are useful in the development and screening of
 CC therapeutically useful compounds. Sequences ABR71793-ABR72097 represent
 CC the human PRO secreted/transmembrane polypeptides of the invention. Note:
 CC The sequence data for this patent is also available in electronic format
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 409 AA;

Query Match 100.0%; Score 409; DB 6; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGVILGALAFQHLNTSDTEGLGVEKGEAKNSITDSQDDVEVYITD 60
 Db 1 MEGESTSAVLGSGVILGALAFQHLNTSDTEGLGVEKGEAKNSITDSQDDVEVYITD 60

QY 61 IQKIYPCVQLPFGFYNSSGEVNEQALKILSNVKNVGVWGYFRHSDQIMTFRERLLHKN 120
 Db 61 IQKIYPCVQLPFGFYNSSGEVNEQALKILSNVKNVGVWGYFRHSDQIMTFRERLLHKN 120

QY 121 LQEHFSDNQLVFLLLTPSIITESCSTHRLHSLYKPKQLFHRVPLVAVNLGMSQGLGYK 180
 Db 121 LQEHFSDNQLVFLLLTPSIITESCSTHRLHSLYKPKQLFHRVPLVAVNLGMSQGLGYK 180

QY 181 TVSGSCMTGFSRAVQTHSSKPFEEGSLKEVHKINEMVYASLOBELKSI CKKVEDSQAV 240
 Db 181 TVSGSCMTGFSRAVQTHSSKPFEEGSLKEVHKINEMVYASLOBELKSI CKKVEDSQAV 240

QY 241 DKLVDVNLKREIEKRRGAQIQAAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
 Db 241 DKLVDVNLKREIEKRRGAQIQAAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300

QY 301 LKRVHVSCKSCYNHHLVDVNLTLVMEHTDIPASPASTPQIHKKALDLDRAQPKRS 360
 Db 301 LKRVHVSCKSCYNHHLVDVNLTLVMEHTDIPASPASTPQIHKKALDLDRAQPKRS 360

QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGFGRSPTF 409
 Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGFGRSPTF 409

RESULT 80

ID ABUS9229

XX ABUS9229 standard; protein; 409 AA.

XX AC ABUS9229;

XX DT 22-APR-2003 (first entry)

XX DE Human secreted/transmembrane protein, #59.
 XX KW Human; PRO; secreted; transmembrane; pharmaceutical; diagnostic;
 XX KW biosensor; bio-reactor; tumour; therapeutic; gene therapy;
 KW tumour-associated antigenic target; TAT; ADAPT;
 KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.
 XX OS Homo sapiens.
 XX PN US2003027162-A1.
 XX PD 06-FEB-2003.
 XX PP 15-NOV-2001; 2001US-00997428.
 XX PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075345P.
 PR 28-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 03-JUN-1998; 98US-0088555P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089633P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 19-JUN-1998; 98US-0089947P.
 PR 19-JUN-1998; 98US-0089948P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090252P.
 PR 23-JUN-1998; 98US-0090254P.
 PR 23-JUN-1998; 98US-0090349P.

PR	23-JUN-1998;	98US-00903555P.	PR	26-AUG-1998;	98US-0098014P.	Qy	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	24-JUN-1998;	98US-0090429P.	PR	31-AUG-1998;	98US-0098525P.	Db	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	24-JUN-1998;	98US-0090431P.	PR	16-SEP-1998;	98US-0100634P.	Qy	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	24-JUN-1998;	98US-0090433P.	PR	16-SEP-1998;	98US-0100634P.	Db	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	24-JUN-1998;	98US-0090444P.	PR	17-SEP-1998;	98US-0100858P.	Qy	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	24-JUN-1998;	98US-0090445P.	PR	17-SEP-1998;	98US-0100858P.	Db	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	24-JUN-1998;	98US-0090472P.	PR	07-OCT-1998;	98US-0100858P.	Qy	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	24-JUN-1998;	98US-0090472P.	PR	07-OCT-1998;	98US-0100858P.	Db	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	24-JUN-1998;	98US-0090533P.	PR	01-DEC-1998;	98US-0100858P.	Qy	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	24-JUN-1998;	98US-0090540P.	PR	01-DEC-1998;	98US-0100858P.	Db	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	24-JUN-1998;	98US-0090542P.	PR	02-DEC-1998;	98US-0100858P.	Qy	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	24-JUN-1998;	98US-0090557P.	PR	02-DEC-1998;	98US-0100858P.	Db	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	24-JUN-1998;	98US-0090567P.	PR	08-MAR-1999;	99US-0123957P.	Qy	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	24-JUN-1998;	98US-0090567P.	PR	08-MAR-1999;	99US-0123957P.	Db	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	25-JUN-1998;	98US-0090678P.	PR	12-MAR-1999;	99US-0123957P.	Qy	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	25-JUN-1998;	98US-0090690P.	PR	12-MAR-1999;	99US-0123957P.	Db	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	25-JUN-1998;	98US-0090694P.	PR	23-JUN-1999;	99US-0141037P.	Qy	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	25-JUN-1998;	98US-0090695P.	PR	23-JUN-1999;	99US-0141037P.	Db	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	25-JUN-1998;	98US-0090696P.	PR	07-JUL-1999;	99US-01443048P.	Qy	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	25-JUN-1998;	98US-0090696P.	PR	07-JUL-1999;	99US-01443048P.	Db	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	25-JUN-1998;	98US-0090696P.	PR	20-JUL-1999;	99US-0144758P.	Qy	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	25-JUN-1998;	98US-0090696P.	PR	20-JUL-1999;	99US-0144758P.	Db	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	26-JUN-1998;	98US-0090862P.	PR	28-JUL-1999;	99US-0146222P.	Qy	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	26-JUN-1998;	98US-0090863P.	PR	28-JUL-1999;	99US-0146222P.	Db	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	01-JUL-1998;	98US-0091360P.	PR	17-AUG-1999;	99US-0149396P.	Qy	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	01-JUL-1998;	98US-0091544P.	PR	17-AUG-1999;	99US-0149396P.	Db	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	02-JUL-1998;	98US-0091478P.	PR	15-SEP-1999;	99US-0149396P.	Qy	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	02-JUL-1998;	98US-0091519P.	PR	15-SEP-1999;	99US-0149396P.	Db	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	02-JUL-1998;	98US-0091626P.	PR	08-OCT-1999;	99US-0158663P.	Qy	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	02-JUL-1998;	98US-0091628P.	PR	08-OCT-1999;	99US-0158663P.	Db	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	02-JUL-1998;	98US-0091633P.	PR	30-NOV-1999;	99US-0158663P.	Qy	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	02-JUL-1998;	98US-0091646P.	PR	30-NOV-1999;	99US-0158663P.	Db	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	02-JUL-1998;	98US-0091673P.	PR	01-DEC-1999;	99US-0158663P.	Qy	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	07-JUL-1998;	98US-0091978P.	PR	01-DEC-1999;	99US-0158663P.	Db	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	07-JUL-1998;	98US-0091982P.	PR	16-DEC-1999;	99US-0158663P.	Qy	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	09-JUL-1998;	98US-0092182P.	PR	16-DEC-1999;	99US-0158663P.	Db	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	09-JUL-1998;	98US-0092182P.	PR	20-DEC-1999;	99US-0158663P.	Qy	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	10-JUL-1998;	98US-0092472P.	PR	20-DEC-1999;	99US-0158663P.	Db	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	20-JUL-1998;	98US-0093339P.	PR	05-JAN-2000;	2000WO-US000219.	Qy	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	30-JUL-1998;	98US-0094651P.	PR	05-JAN-2000;	2000WO-US000219.	Db	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	04-AUG-1998;	98US-0095282P.	PR	18-FEB-2000;	2000WO-US0003565.	Qy	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	04-AUG-1998;	98US-0095285P.	PR	18-FEB-2000;	2000WO-US0003565.	Db	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	04-AUG-1998;	98US-0095301P.	PR	22-FEB-2000;	2000WO-US0004414.	Qy	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	04-AUG-1998;	98US-0095318P.	PR	22-FEB-2000;	2000WO-US0004414.	Db	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	04-AUG-1998;	98US-0095321P.	PR	24-FEB-2000;	2000WO-US0005004.	Qy	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	04-AUG-1998;	98US-0095325P.	PR	24-FEB-2000;	2000WO-US0005004.	Db	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	10-AUG-1998;	98US-0095916P.	PR	02-MAR-2000;	2000WO-US0005841.	Qy	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	10-AUG-1998;	98US-0095929P.	PR	02-MAR-2000;	2000WO-US0005841.	Db	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	10-AUG-1998;	98US-0096012P.	PR	15-MAR-2000;	2000WO-US0006884.	Qy	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	11-AUG-1998;	98US-0096143P.	PR	15-MAR-2000;	2000WO-US0006884.	Db	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
PR	11-AUG-1998;	98US-0096146P.	PR	30-MAR-2000;	2000WO-US0008439.	Qy	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	12-AUG-1998;	98US-0096329P.	PR	30-MAR-2000;	2000WO-US0008439.	Db	1	MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEYKGAKNISITDSQMDDEVVYTTID	60
PR	17-AUG-1998;	98US-0096757P.	PR	17-MAY-2000;	2000WO-US013705.	Qy	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	17-AUG-1998;	98US-0096766P.	PR	17-MAY-2000;	2000WO-US013705.	Db	61	IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGWYKPRHSDQIMTFERLLHKN	120
PR	17-AUG-1998;	98US-0096773P.	PR	22-MAY-2000;	2000WO-US014042.	Qy	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	17-AUG-1998;	98US-0096791P.	PR	22-MAY-2000;	2000WO-US014042.	Db	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
PR	17-AUG-1998;	98US-0096867P.	PR	30-MAY-2000;	2000WO-US014941.	Qy	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	17-AUG-1998;	98US-0096891P.	PR	30-MAY-2000;	2000WO-US014941.	Db	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
PR	17-AUG-1998;	98US-0096894P.	PR	02-JUN-2000;	2000WO-US015264.	Qy	241	DKLVKDVNRLKREIEKRGGAQIOAAREKNIQKQPOENIFLQALRTFFPNSEFLHSCVMS	300
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PR	18-AUG-1998;	98US-0096960P.	PR	11-AUG-2000;	2000WO-US022031.	Qy	121	LOEHFSNQDLVFLLLTPSIITSCSTHRLSHLYKPKQGLFHRVPLVYANLGMSEQLGYK	180
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PR	19-AUG-1998;	98US-0097141P.	PR	23-AUG-2000;	2000WO-US023522.	Db	181	TVSGSCMSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMIASLOBELKSI CKKVEDSQA	240
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XX
AC ABU85339;
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DT 02-JUL-2003 (first entry)
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KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; TNF-alpha;
KW tumour necrosis factor-alpha; chondrocyte cell.
XX
OS Homo sapiens.
XX
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XX
PD 30-JAN-2003.
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PF 19-JUN-2002; 2002US-00175752.
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QY 181 TVSGSCWSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASIQEELKSIKKVEDSEQAV 240
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XX AC ABU89029;
XX DT 08-JUL-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #67.
KW Human; secreted protein; transmembrane protein; PRO;
KW tumour necrosis factor-alpha; TNF-alpha; blood; tumour;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW adrenal tumour; lung tumour; colon tumour; breast tumour; gene therapy;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW bone disorder; cartilage disorder; sports injury; arthritis; cytostatic;
KW antiarthritic; osteopathic.
OS Homo sapiens.
PN US2003022297-A1.
XX 30-JAN-2003.
XX 20-JUN-2002; 2002US-00176757.
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Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEGESTSAVLGFGVLGALAFQHLNTDSDTEGFLLEGVKGEAKNSITDSQDDVEVVYITD 60

QY 61 IQKIYPCYOLFQFYNSSGVEVNEQALKKILSNVKNVGVGKYKPRRSHSDQIMTFRERLLHKN 120
DB 61 IQKIYPCYOLFQFYNSSGVEVNEQALKKILSNVKNVGVGKYKPRRSHSDQIMTFRERLLHKN 120

QY 121 LQEHFNSQDLVLLLTTPSIITSCSTHRLHSLYKPKGLFHRVPLVNVANLGMSEQLGYK 180
DB 121 LQEHFNSQDLVLLLTTPSIITSCSTHRLHSLYKPKGLFHRVPLVNVANLGMSEQLGYK 180

QY 181 TVSGSCMSGTFGRVOTHSKFEEDGSLKEVHKINEMVASYLQEBLKSIKKVEDSEQAV 240
DB 181 TVSGSCMSGTFGRVOTHSKFEEDGSLKEVHKINEMVASYLQEBLKSIKKVEDSEQAV 240

QY 241 DKLVKDVNLRKREIEKRRGAQIQAREKNIQKDPENIFLCOALRTFFPNSFFLHSCVMS 300
DB 241 DKLVKDVNLRKREIEKRRGAQIQAREKNIQKDPENIFLCOALRTFFPNSFFLHSCVMS 300

QY 301 LKNRHSVSKSCNVNHLVDVNDITLNVHTDIPASASTPQIILKHKALDLDNRQFKRS 360
DB 301 LKNRHSVSKSCNVNHLVDVNDITLNVHTDIPASASTPQIILKHKALDLDNRQFKRS 360

QY 361 RLIDTDQKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSPTF 409
DB 361 RLIDTDQKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYSRSPTF 409

RESULT 83
ABU83109
ID ABU83109 standard; protein; 409 AA.
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AC ABU83109;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) #67.
XX
KW Human; cytotatic; secreted and transmembrane protein; PRO;
KW chromosome mapping; gene mapping; gene therapy;
KW tumour necrosis factor alpha; TNF-alpha; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN US2003032105-A1.
XX
PD 13-FEB-2003.
XX
PF 18-JUN-2002; 2002US-00174585.
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Best Local Similarity 100.0%; Pred. No. 0;
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Qy	61	IQKYPICYQLFSFYNSSGEVNEQALKILSNVKNVVGWYKFRHSDQIMTFRERLIHKN	120
Db	61	IQKYPICYQLFSFYNSSGEVNEQALKILSNVKNVVGWYKFRHSDQIMTFRERLIHKN	120
Qy	121	LOEHFSNODLVFLLLTPSIITSCSTHRLHSLYKPKQGLFHRVPLVWNLGMSQLGYK	180
Db	121	LOEHFSNODLVFLLLTPSIITSCSTHRLHSLYKPKQGLFHRVPLVWNLGMSQLGYK	180
Qy	181	TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASLOBELKSICKKVEDSEQAV	240
Db	181	TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASLOBELKSICKKVEDSEQAV	240
Qy	241	DKLVKDVNRLKREIKRGAQIQAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCWMS	300
Db	241	DKLVKDVNRLKREIKRGAQIQAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCWMS	300
Qy	301	LKNRHSKSSCNTNHHLDVVNDLTLVVEHTDIPASPASTPQIIKKALDLDORWQFKRS	360
Db	301	LKNRHSKSSCNTNHHLDVVNDLTLVVEHTDIPASPASTPQIIKKALDLDORWQFKRS	360
Qy	361	RLLDQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGESRSPTF	409
Db	361	RLLDQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGESRSPTF	409

RESULT 84
ABU94965
ID ABU94965 standard; protein; 409 AA.
XX AC ABU94965;
XX DT 24-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1013.
XX KW Human; secreted and transmembrane protein: PRO; cytostatic; gene therapy;
KW tumour.

XX OS Homo sapiens.
XX PN US2003032123-A1.
XX PD 13-FEB-2003.
XX PF 25-JUN-2002; 2002US-00180555.
XX PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
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DB 121 LOEHFSNODLVLLTPSIITESTCSHLEHSLYKPKGLPHRYPLVAVNLGMSEQLGYK 180
QY 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSI CKKVEDSQAQV 240
DB 181 TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSI CKKVEDSQAQV 240
QY 241 DKLVDVNRLLKREIEKRGAGIQAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLLKREIEKRGAGIQAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRVHSSKSNYNHHLVDVNLTLWVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
DB 301 LKNRVHSSKSNYNHHLVDVNLTLWVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
QY 361 RLITQDKRSKANTGSSNODKASKMSSPETDEEIEKMGKGFGEYSRPTTF 409
DB 361 RLITQDKRSKANTGSSNODKASKMSSPETDEEIEKMGKGFGEYSRPTTF 409
RESULT 86
ASUB84024
ID ABUB84024 standard; protein; 409 AA.
XX AC
XX ABUB84024;
XX DT 11-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #67.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; cytostatic.
XX OS Homo sapiens.
XX PN US2003032111-A1.
XX PD 13-FEB-2003.
XX PF 20-JUN-2002; 2002US-00176493.
XX PR 18-SEP-1997; 97US-005263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
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PR 01-APR-1998; 98US-0080327P.
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PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
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PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 IQYIPCYQLFSYNSGVEVNEQALKILSNVKNVGVYKFRHSQDQMTFRELLHKN 120
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Qy 121 LQEHFNSQDLVFLLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVWNLGMSQLGYK 180
Db 121 LQEHFNSQDLVFLLLTPSIITSCSTRLEHSLYKPKGLFHRVPLVWNLGMSQLGYK 180

Qy 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIOBELKSTCKKVEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASIOBELKSTCKKVEDSEQAV 240

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Qy 301 LKRVHVSQSCNHNLDVVDNLTLMVETDIPASPASTPOIKKALDLDLRQOFKRS 360
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Qy 361 RLDDTQKRSKANTGSSNODKASKMSSPETDEIEKMGFGFYSPPTF 409
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RESULT 87
ABU93675
ID ABU93675 standard; protein; 409 AA.
XX AC ABU93675;
XX DT 11-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1013.
XX KW Human; gene therapy; chondrocyte stimulator; tumour; TNF-alpha;
XX KW tumour Necrosis factor alpha.
XX OS Homo sapiens.
XX FN US2003032119-A1.
XX PD 13-FEB-2003.
XX PF 25-JUN-2002; 2002US-00180544.
XX PR 26-JUN-1998; 98US-00105413.
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PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.


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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US021508.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006684.
PR 20-MAR-2000; 2000WO-US007377.
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PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WJ,
PI Zhang Z;
XX
XX WPI; 2003-340824/32.
DR N-PSDB; ACD44240.
DR
XX
XX Novel isolated PRO polypeptides e.g., PRO825, PRO1068, PRO1184, PRO1346
PI and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT and are therapeutically useful for enhancing immune responses.
XX
XX Claim 12; Fig 95; 661pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. ABO25891-
CC ABO26037 represent the human PRO polypeptides of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/paipsDIDentry.html
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PR	04-JUL-1998;	98US-0094006P.	QY	181	TVSGSCMSTGFSRAVQTHSKFEDGSLKEVHKINEMVYASLOEBLKICKKVEDSEQAV	240
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PR	16-SEP-1998;	98US-0101933P.	QY			
PR	17-SEP-1998;	98US-0100683P.	Db			
PR	17-SEP-1998;	98US-0100694P.	QY			
PR	17-SEP-1998;	98US-0100919P.	Db			
PR	17-SEP-1998;	98US-0100930P.	QY			
PR	17-SEP-1998;	98US-0100849P.	Db			
PR	18-SEP-1998;	98US-0101014P.	QY			
PR	18-SEP-1998;	98US-0101068P.	Db			
PR	23-SEP-1998;	98US-0101471P.	QY			
PR	23-SEP-1998;	98US-0101472P.	Db			
PR	23-SEP-1998;	98US-0101475P.	QY			
PR	23-SEP-1998;	98US-0101477P.	Db			
PR	24-SEP-1998;	98US-0101738P.	QY			
PR	24-SEP-1998;	98US-0101739P.	Db			
PR	24-SEP-1998;	98US-0101743P.	QY			
PR	24-SEP-1998;	98US-0101922P.	Db			
PR	25-SEP-1998;	98US-0101786P.	QY			
PR	29-SEP-1998;	98US-0102207P.	Db			
PR	29-SEP-1998;	98US-0102240P.	QY			
PR	29-SEP-1998;	98US-0102330P.	Db			
PR	29-SEP-1998;	98US-0102331P.	QY			
PR	30-SEP-1998;	98US-0102467P.	Db			
PR	30-SEP-1998;	98US-0102570P.	QY			
PR	30-SEP-1998;	98US-0102571P.	Db			
PR	01-OCT-1998;	98US-0102654P.	QY			
PR	01-OCT-1998;	98US-0102657P.	Db			
PR	01-OCT-1998;	98US-0102658P.	QY			

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLGGVFLGALAFQHINTSDTEGFLGVEKGAKNISITDSQMDVVEVYITD 60
Db 1 MEGESTSAVLGGVFLGALAFQHINTSDTEGFLGVEKGAKNISITDSQMDVVEVYITD 60

RESULT 90
ABO27291
ID ABO27291 standard; protein; 409 AA.
XX AC ABO27291;
XX AC ABO27291;
DT 11-SEP-2003 (first entry)
DE Human secreted/transmembrane polypeptide PRO1013.
XX Human; tumour; cancer; gene therapy; tissue typing.
XX Homo sapiens.
XX OS
XX PN US20030095012-A1.
XX PD 09-JAN-2003.
XX PF 01-MAY-2002; 2002US-00063517.
XX 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WC-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WC-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 18-FEB-1999; 99WC-US031274.
PR 18-FEB-2000; 2000WC-US004341.
PR 01-MAR-2000; 2000WC-US005601.
PR 02-MAR-2000; 2000WC-US005841.
PR 21-MAR-2000; 2000WC-US007532.
PR 22-MAY-2000; 2000WC-US014042.
PR 02-JUN-2000; 2000WC-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WC-US023328.
PR 18-SEP-2000; 2000US-0064610.
PR 18-SEP-2000; 2000US-0065350.
PR 08-NOV-2000; 2000US-0079238.
PR 10-NOV-2000; 2000WC-US030873.
PR 01-DEC-2000; 2000WC-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WC-US034956.
PR 28-FEB-2001; 2001WC-US006520.

PR 22-MAR-2001; 2001US-00815744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 23-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006857.
XX
XX (GETH) GENENTECH INC.
PA
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-447383/42.
DR N-PSDB; ACD45159.
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.
XX
XX Disclosure; Fig 22; 223pp; English.
XX
XX The invention relates to an antibody that binds to a secreted and
CC transmembrane PRO polypeptide. The methods and compositions of the
CC present invention are useful for the preparation of a medicament for the
CC treatment of disorders associated with the aberrant expression or
CC activity of the PRO polypeptide, such as tumor conditions and cancer.
CC They can also be used to generate transgenic or knockout animals useful
CC in the development and screening of therapeutically useful reagents. The
CC PRO polypeptides and encoding nucleic acids can be used as molecular
CC weight markers for protein electrophoresis, chromosome identification and
CC tissue typing. The antibodies may be used in various diagnostic,
CC competitive binding and/or immunoprecipitation assays. The present
CC sequence represents the amino acid sequence of a secreted and
CC transmembrane PRO polypeptide
XX
XX Sequence 409 AA;

Query Match 100.0%; Score 409; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60
Db 1 MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDVVEVYITD 60

QY 61 IQYIPCYQLFSFYNSGGEVNEQALKILSNVKNVGVGKFRHSDQIMTFRLLHKN 120
Db 61 IQYIPCYQLFSFYNSGGEVNEQALKILSNVKNVGVGKFRHSDQIMTFRLLHKN 120

QY 121 LQEHFNSQDLVFLLLTPSIITESCSTRLEHSLYKPKGLFHRVPLVAVNLGMSQOLGYK 180
Db 121 LQEHFNSQDLVFLLLTPSIITESCSTRLEHSLYKPKGLFHRVPLVAVNLGMSQOLGYK 180

QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASLQEEKLSICKKVEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASLQEEKLSICKKVEDSEQAV 240

QY 241 DKLVDVNLKRIEKRGQAIOAAREKNIOKDPQENIFLCOALRTFFNSRFLHSCVMS 300
Db 241 DKLVDVNLKRIEKRGQAIOAAREKNIOKDPQENIFLCOALRTFFNSRFLHSCVMS 300

QY 301 LKNRHVSNSNNHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDLRWQFKKS 360
Db 301 LKNRHVSNSNNHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDLRWQFKKS 360

QY 361 RLDTQDKRKANTGSSNQKASKMSSPETDEIEKMKGGEYSRSPTF 409
Db 361 RLDTQDKRKANTGSSNQKASKMSSPETDEIEKMKGGEYSRSPTF 409

RESULT 91
ABR68752
ID ABR68752 standard; protein; 409 AA.
XX
AC ABR68752;
XX
XX 11-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1013, SEQ ID NO:134.
XX
XX Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003027271-A1.
XX
XX 06-FEB-2003.
XX
XX 21-JUN-2002; 2002US-00176488.
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XX 18-SEP-1997; 97US-0059263P.
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PR 21-OCT-1997; 97US-0083486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
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PR 17-DEC-1997; 97US-0069870P.
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PR	22-MAY-1998;	98US-0086486P.	PR	26-AUG-1998;	98US-0097552P.
PR	22-MAY-1998;	98US-0087098P.	PR	26-AUG-1998;	98US-0097555P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097711P.
PR	02-JUN-1998;	98US-0087603P.	PR	26-AUG-1998;	98US-0097974P.
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PR	03-JUN-1998;	98US-0087827P.	PR	01-SEP-1998;	98US-0098716P.
PR	04-JUN-1998;	98US-0088025P.	PR	01-SEP-1998;	98US-0098723P.
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PR	05-JUN-1998;	98US-0088212P.	PR	10-SEP-1998;	98US-0099763P.
PR	05-JUN-1998;	98US-0088217P.	PR	15-SEP-1998;	98US-0099812P.
PR	09-JUN-1998;	98US-0088655P.	PR	15-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088722P.	PR	16-SEP-1998;	98US-0100622P.
PR	10-JUN-1998;	98US-0088738P.	PR	16-SEP-1998;	98US-0100864P.
PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0101751P.
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PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100930P.
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PR	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101477P.
PR	17-JUN-1998;	98US-0089653P.	PR	23-SEP-1998;	98US-0101738P.
PR	18-JUN-1998;	98US-0089908P.	PR	24-SEP-1998;	98US-0101739P.
PR	18-JUN-1998;	98US-0089952P.	PR	24-SEP-1998;	98US-0101743P.
PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090252P.	PR	25-SEP-1998;	98US-0101786P.
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PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102330P.
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PR	24-JUN-1998;	98US-0090535P.	PR	30-SEP-1998;	98US-0102570P.
PR	24-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090576P.	PR	01-OCT-1998;	98US-0102684P.
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PR	26-JUN-1998;	98US-00105413.			
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PR	26-JUN-1998;	98US-0091010P.			
PR	01-JUL-1998;	98US-0091359P.			
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PR	02-JUL-1998;	98US-0091478P.			
PR	02-JUL-1998;	98US-0091486P.			
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PR	02-JUL-1998;	98US-0091628P.			
PR	02-JUL-1998;	98US-0091632P.			
PR	24-JUL-1998;	98US-0094006P.			

Query Match.
Best Local Similarity 100.0%;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

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Db 181 TVSGSCMTGFRVQTHSSKEFEEDGSLKEVHKINEMVASYLOELKICKVEDSEQAV 240
QY 241 DKLVKDVNLKREIEKRRGAQICAAAREKNIQKDPQENIFLCOALRTFFPNSFLHSCVMS 300
Db 241 DKLVKDVNLKREIEKRRGAQICAAAREKNIQKDPQENIFLCOALRTFFPNSFLHSCVMS 300
QY 301 LKNRHVSKSCNNYHHLVDVNLTLWVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
Db 301 LKNRHVSKSCNNYHHLVDVNLTLWVEHTDIPASPASTPQIIKHKALDLDLDRWQFKRS 360
QY 361 RLILDQDKESKANTGSSNQDKASKMSSPTDEIEKMKGFGEYSRSPTF 409
Db 361 RLILDQDKESKANTGSSNQDKASKMSSPTDEIEKMKGFGEYSRSPTF 409

RESULT 92
ABO06568
ID ABO06568 standard; protein; 409 AA.
XX
AC ABO06568;
XX
DT 17-AUG-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) #67.
XX
KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003036125-A1.
XX
PD 20-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00180999.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
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PR 21-NOV-1997; 97US-0066120P.
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121	LQEHFSNQDLVFLLLTTSITESCSTHRLHSLYKPKQLFHRVPLVWANGMSEQLGYK	180		
121	LQEHFSNQDLVFLLLTTSITESCSTHRLHSLYKPKQLFHRVPLVWANGMSEQLGYK	180		
181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASIOBELKSIKKVEDSEQV	240		
181	TVSGSCMTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASIOBELKSIKKVEDSEQV	240		
241	DKLVKDVNRLKREIEKRRGAQIOAAEKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS	300		
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DT	04-APR-2003 (first entry)			
XX				
DE	Human PRO polypeptide #67.			
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KW	Human; PRO; tumour necrosis factor-alpha; blood; cancer;			
KW	chondrocyte cell; tumour; adrenal tumour; lung; colon; breast; prostate;			
KW	kidney; rectum; cervix; liver; bone disorder; cartilage disorder;			
XX	arthritis; sports injury; genetic disorder; antiarthritic; vulnerary.			
OS				
XX	Homo sapiens.			
XX				
FN	US2003027280-A1.			
XX				
PD	06-FEB-2003.			
XX				

RESULT 94

ABU56997

ID ABU56997 standard; protein; 409 AA.

XX

AC ABU56997;

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DT 04-APR-2003 (first entry)

2014-2015

Human PRO polypeptide #67.

Human: PRO - tumour necrosis;

KW
KW
Human; FRO; tumour necrosis
chondrocyte cell; tumour:
KW

kidney: rectum: cervix: li

arthritis; sports injury;
KW

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SO Homo sapiens.

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PN US2003027280-A1.

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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.

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Best Local Similarity 100.0%; Pred. No. 0;
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Db 1 MEGESTSAVLGGFVLGALAFQHLNTSDTEGFLGEGVKEAKNSITDSQMDDEVVYITD 60

Qy 61 IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGKFRHSDQIMTFRERLLHN 120
Db 61 IQYIPCYQLFSPYNSGGEVNEQALKILSNVKNVGVGKFRHSDQIMTFRERLLHN 120

Qy 121 LOEHFSNODLVFLLTPSIIITESCSTHRLHSYKPKGLFHRVPLVANLGMSEQLGYK 180
Db 121 LOEHFSNODLVFLLTPSIIITESCSTHRLHSYKPKGLFHRVPLVANLGMSEQLGYK 180

Qy 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMYASLOEELKSI CKKVEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMYASLOEELKSI CKKVEDSEQAV 240

Qy 241 DKLYKDVNRLKRETEKERGAQIQAAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
Db 241 DKLYKDVNRLKRETEKERGAQIQAAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300

Qy 301 LKNRVSKSCNYYNHLDVVNDLTLVVEHTDIPASPASTPQIIKKHALDLDWRQPKRS 360
Db 301 LKNRVSKSCNYYNHLDVVNDLTLVVEHTDIPASPASTPQIIKKHALDLDWRQPKRS 360

Qy 361 RLDTQDKRSKANTGSSNQDKASKMSSPETDEEIEKMKGGEYSRSTPF 409
Db 361 RLDTQDKRSKANTGSSNQDKASKMSSPETDEEIEKMKGGEYSRSTPF 409

RESULT 95
ABU85949
ID ABU85949 standard; protein; 409 AA.
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[illegible]

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PR 17-SEP-1998; 98US-0106883P.
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Best Local Similarity 100.0%; Pred.No. 0;
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Db	1	MEGESTSAVLGSGFVLGALAFQHLNLTDSFTGFLGGEVKEAKNSITDSQMDDEVVVTID	60	PR	11-MAR-1998;	98US-0077632P.
QY	61	IQKIYPCVQLSFYNSGEVNEQALKILSNVKNVGVGYKFRHSQDQIMTFRERLLHKN	120	PR	20-MAR-1998;	98US-0078886P.
Db	61	IQKIYPCVQLSFYNSGEVNEQALKILSNVKNVGVGYKFRHSQDQIMTFRERLLHKN	120	PR	27-MAR-1998;	98US-0078939P.
QY	121	LOEHFSNQDLVFLLTPTSIITESCSTHLESHLYKPKQGLFHRVPLVNVANLGMSEQLGYK	180	PR	27-MAR-1998;	98US-0079664P.
Db	121	LOEHFSNQDLVFLLTPTSIITESCSTHLESHLYKPKQGLFHRVPLVNVANLGMSEQLGYK	180	PR	31-MAR-1998;	98US-0080107P.
QY	181	TVSGSCMTGFRSAVQTHSSKFFEDGSLKEVHKINENYASIQBELKSI CKKVEDSEQAV	240	PR	31-MAR-1998;	98US-0080194P.
Db	181	TVSGSCMTGFRSAVQTHSSKFFEDGSLKEVHKINENYASIQBELKSI CKKVEDSEQAV	240	PR	01-APR-1998;	98US-0080327P.
QY	241	DKLVKDVNRLKREIEKRGGAQIQAAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS	300	PR	01-APR-1998;	98US-0080333P.
Db	241	DKLVKDVNRLKREIEKRGGAQIQAAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS	300	PR	08-APR-1998;	98US-0080333P.
QY	301	LKNRVSKSSCNYNHLDVVDNLTLWVHTDIPASPASTPQIIKHKALDLDLDRWQFKRS	360	PR	08-APR-1998;	98US-0081049P.
Db	301	LKNRVSKSSCNYNHLDVVDNLTLWVHTDIPASPASTPQIIKHKALDLDLDRWQFKRS	360	PR	09-APR-1998;	98US-0081195P.
QY	361	RLLDTDQKRSKANTGSSNODKASKNMSPTTDEEIEKMGFGGEYSRSPTF	409	PR	15-APR-1998;	98US-0081838P.
Db	361	RLLDTDQKRSKANTGSSNODKASKNMSPTTDEEIEKMGFGGEYSRSPTF	409	PR	21-APR-1998;	98US-0082568P.
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KW chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;					29-APR-1998;	98US-0083499P.
KW prostate; rectal; cervical; liver; cancer; cytostatic.					29-APR-1998;	98US-0083559P.
OS Homo sapiens.					05-MAY-1998;	98US-0084366P.
XX US2003036138-A1.					06-MAY-1998;	98US-0084414P.
XX 20-FEB-2003.					07-MAY-1998;	98US-0084639P.
XX 28-JUN-2002; 2002US-00184650.					07-MAY-1998;	98US-0084640P.
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XX 28-OCT-1997;					22-MAY-1998;	98US-0086486P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
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Query Match 100.0%; Score 409; DB 6; Length 409;
Best local similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGFVLGALAFQHLNTSDTEGFLGEGVKEAKNSITDSQMDVVEVYITD 60
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QY 121 LQEHFSNQDLVFLLLTPSIIITSCSTRLEHSLYKPKGLFHRVPLVWANGMSQOLGYK 180
DB 121 LQEHFSNQDLVFLLLTPSIIITSCSTRLEHSLYKPKGLFHRVPLVWANGMSQOLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKPFEEGSLKEVHKINEMVASYLQEEELKSIKKVVESEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKPFEEGSLKEVHKINEMVASYLQEEELKSIKKVVESEQAV 240
QY 241 DKLVDVNRKREIEKRRGAQIOAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDVNRKREIEKRRGAQIOAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
QY 301 LKQHVSKSCNHNHLDVVDNLTLVHTDIPASPASTPOI IKHKLDDDRNQFKRS 360
DB 301 LKQHVSKSCNHNHLDVVDNLTLVHTDIPASPASTPOI IKHKLDDDRNQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSRPTF 409
DB 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSRPTF 409

RESULT 98
ASU83719
ID ABU83719 standard; protein; 409 AA.
XX AC ABU83719;
XX DT 11-AUG-2003 (first entry)
XX DR Human secreted/transmembrane protein (PRO) #67.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX OS tissue typing; cytostatic.
XX OS Homo sapiens.
XX PN US2003032109-A1.
XX PD 13-FEB-2003.
XX PF 20-JUN-2002; 2002US-00176485.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 21-OCT-1997; 97US-0063486P.
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XX	Human; PRO; secreted polypeptide; transmembrane polypeptide; cytostatic;
KW	tumour necrosis factor-alpha; TNF-alpha; Blood; tumour; chondrocyte cell;
KW	cancer.
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XX	Homo sapiens.
OS	
XX	US2003040066-A1.
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XX	26-JUN-2002; 2002US-00183019.
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PR	07-OCT-1998	98US-0103497P

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QY	241	DKLVKDVNRLKREIEKRGAGIQAAAEKNI QKQPQENI FLCQALRTPFFNSFPLHSCVMS	300
DB	241	DKLVKDVNRLKREIEKRGAGIQAAAEKNI QKQPQENI FLCQALRTPFFNSFPLHSCVMS	300
QY	301	LKNRHVS KSCYNVNHLDVVDNITLWVHEHTIDIPEASPASTPQIIKHKALDLDLRWQFKS	360

DB 301 LKNRHSKSNYNHLDVVDNLTLVVEHTDIPASPASTPQIIKHKALDLDNRQFKRS 360
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DB 361 RLIDTQDKRSKANTGSSNQDKASKMSPTDEIEKMKGFGEYSRSPTF 409
RESULT 100
ABU92486
ID ABU92486 standard; protein; 409 AA.
XX AC ABU92486;
XX DT 17-JUL-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO1013.
XX KW Human; PRO; secreted protein; transmembrane protein; cytostatic;
KW vulnery; osteopathic; antiarthritic; antirheumatic; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tumour necrosis factor; pericyte cell proliferation;
KW TNF-alpha; proteoglycans release; cartilage; cancer; wound healing;
KW cartilage defect; osteoarthritis; rheumatoid arthritis.
XX OS Homo sapiens.
XX PN US2003045684-A1.
XX PD 06-MAR-2003.
XX EF 02-MAY-2002; 2002US-00063553.
XX PR 30-DEC-1998; 98KP-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 25-AUG-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAR-2000; 2000WO-US014042.
PR 22-AUG-2000; 2000WO-US015264.
PR 24-AUG-2000; 2000US-00644848.
PR 18-SEP-2000; 2000US-00664610.
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PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US0006520.
PR 22-MAR-2001; 2001US-00815744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 28-JUL-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
(GETH) GENENTECH INC.

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WT;
XX WPI; 2003-392892/37.
DR N-PSDB; ACA93707.
XX
PT New PRO994 polypeptide, useful for detecting tumors, or for stimulating
PT Tumor Necrosis Factor alpha, or pericyte proliferation, especially for
PT treating cancer, cartilage defects, osteoarthritis and rheumatoid
PT arthritis in a mammal.
XX
PS Disclosure; Fig 22; 235pp; English.
XX
CC The invention relates to a new isolated PRO994 polypeptide comprises an
CC amino acid sequence appearing as ABU92499, PRO994 lacking its associated
CC signal peptide, the extracellular domain of PRO994, the extracellular
CC domain of PRO994 (lacking its associated signal peptide) or the protein
CC encoded by the full-length coding sequence of the cDNA ATCC 203018. Also
CC included is a chimaeric molecule comprising the PRO994 polypeptide fused
CC to a heterologous amino acid sequence. The PRO polypeptide is useful in
CC pharmaceuticals, diagnostics, biosensors or bioreactors. It is
CC particularly useful for detecting tumors (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood, for stimulating the proliferation of pericyte
CC cells, or stimulating the release of proteoglycans from cartilage. The
CC polypeptide may be employed for a variety of therapeutic purposes, e.g.
CC for treating cancer, wound healing, cartilage defects, osteoarthritis,
CC rheumatoid arthritis. Also disclosed are the cDNA encoding PRO994, 83,
CC other PRO polypeptides and their encoding cDNAs. The present sequence
CC represents a PRO polypeptide of the invention
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: April 16, 2004, 10:19:09
Job time : 85 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:15:05 ; Search time 17 seconds
(without alignments)
1252.747 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 409

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 6

Total number of hits satisfying chosen parameters: 941

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	8	2.0	199	1 PVA STRP3	Q8k7h6 streptococc
2	8	2.0	199	1 PVA STRP8	Q8p120 streptococc
3	8	2.0	199	1 PVA STRP1	Q92zn9 streptococc
4	8	2.0	612	1 DNAK LISIN	Q92bn8 listeria in
5	8	2.0	612	1 DNAK LISMO	Q92bn8 listeria mo
6	8	2.0	1138	1 PGFI MOUSE	Q8chg7 mus musculu
7	8	2.0	1226	1 KF4A XENLA	Q91784 xenopus lae
8	8	2.0	1499	1 PGFI HUMAN	Q91784 xenopus lae
9	7	1.7	184	1 SUG PRODU	P20928 proteus vul
10	7	1.7	105	1 SUG CITFR	P20928 proteus vul
11	7	1.7	153	1 PTGN BRAJA	O69279 citrobacter
12	7	1.7	157	1 YTFN BACSU	P30335 bradyrhizob
13	7	1.7	165	1 YGUE YEAST	O32068 bacillus su
14	7	1.7	182	1 VB07 VACCV	P53095 saccharomyc
15	7	1.7	216	1 Y458 METJA	P21003 vaccinia vi
16	7	1.7	221	1 GPX5 CANFA	O57900 methanococc
17	7	1.7	242	1 MPGR PYRFU	O46607 canis fami
18	7	1.7	247	1 SURE NITEU	Q8u381 pyrococcus
19	7	1.7	256	1 Y727 METTH	Q82vv9 nitrosomona
20	7	1.7	282	1 YCS3 METJA	O26823 methanobact
21	7	1.7	294	1 OSTP MOUSE	Q58650 methanococc
22	7	1.7	296	1 OSB1 BORBU	P10923 mus musculu
23	7	1.7	306	1 COAA STRP3	P17739 borrelia bu
24	7	1.7	306	1 COAA STRP8	Q8k7c7 streptococc
25	7	1.7	306	1 COAA STRP1	Q850v9 streptococc
26	7	1.7	308	1 Y040 BPT4	Q852h1 streptococc
27	7	1.7	322	1 OZB2 HUMAN	P39254 bacterioph
28	7	1.7	331	1 RBGR BACHD	Q8ngil homo sapien
29	7	1.7	339	1 KDGT ERWCH	Q9k6k2 bacillus ha
30	7	1.7	345	1 RDS2 XENLA	P15701 erwinia chr
31	7	1.7	363	1 PG41 COLLN	O42582 xenopus lae
32	7	1.7	385	1 NUPM METSE	O00446 colletoctric
33	7	1.7	413	1 YG18 AQUAE	O47495 metridium s
					O67545 aquifex aeo

34	7	1.7	465	1 GAC1 HUMAN	Q8n1c3 homo sapien
35	7	1.7	474	1 DLDH HALVO	Q04829 halobacteri
36	7	1.7	478	1 IF3Y YEAST	P41814 saccharomyc
37	7	1.7	486	1 MURC VIBCH	Q9kpg8 vibrio chol
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48	7	1.7	638	1 DNAS BACTN	Q89v46 bacteroides
49	7	1.7	755	1 SENS HUMAN	Q96hi0 homo sapien
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53	7	1.7	954	1 M3KA HUMAN	Q02779 homo sapien
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55	7	1.7	1142	1 PAK1 YEAST	P38990 saccharomyc
56	7	1.7	1178	1 PYC1 YEAST	P11154 saccharomyc
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58	7	1.7	1341	1 VG37 BPT2	P07067 bacterioph
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60	7	1.7	1632	1 UN89 CAEEL	O01761 caenorhabdi
61	6	1.5	29	1 KDPE ECOLI	P36937 escherichia
62	6	1.5	38	1 YC69 HAEIN	P44148 haemophilus
63	6	1.5	52	1 TPCS PRODO	P81074 prototenus
64	6	1.5	58	1 68MP HUMAN	P56378 homo sapien
65	6	1.5	58	1 68MP MOUSE	P56379 mus musculu
66	6	1.5	60	1 68MP BOVIN	P14790 bos taurus
67	6	1.5	66	1 Y766 METJA	Q58176 methanococc
68	6	1.5	68	1 Y055 NPVOP	O10313 orgyia pseu
69	6	1.5	78	1 U197 DROME	Q9vva8 drosophila
70	6	1.5	79	1 Y607 METJA	Q58024 methanococc
71	6	1.5	83	1 OAD3 KLEPN	P13155 klebsiella
72	6	1.5	93	1 DEP2 MOUSE	P28309 mus musculu
73	6	1.5	103	1 RM32 SCHPO	Q84379 schizosacch
74	6	1.5	110	1 Y182 STRCO	P19781 streptomyce
75	6	1.5	110	1 YU44 PYRAE	Q8ztv7 pyrobaculum
76	6	1.5	111	1 RL30 ORYSA	Q9edg6 oryza sativ
77	6	1.5	112	1 RL30 EUPES	Q9m5m6 euphorbia e
78	6	1.5	112	1 RL30 LUPLU	O49884 lupinus lut
79	6	1.5	112	1 RL30 MAIZE	O48558 zea mays (m
80	6	1.5	114	1 YU74 AQUAE	O67784 aquifex aeo
81	6	1.5	116	1 NU3M SQUAC	Q92z47 squalus aca
82	6	1.5	117	1 AMC2 FIG	P22952 sus scrofa
83	6	1.5	120	1 Y555 PYRHO	O59124 pyrococcus
84	6	1.5	122	1 ZEAV MAIZE	P05815 zea mays (m
85	6	1.5	125	1 PFDB HALN1	Q9hsh0 halobacteri
86	6	1.5	126	1 Y576 HAEIN	P44762 haemophilus
87	6	1.5	126	1 YB01 PASMU	Q9clv1 pasteurilla
88	6	1.5	129	1 RS11 NITEU	Q82x71 nitrosomona
89	6	1.5	129	1 V132 FOWPV	P15914 fowipox vir
90	6	1.5	131	1 YN09 YEAST	P53841 saccharomyc
91	6	1.5	134	1 RVUX HELPY	O25101 helicobacte
92	6	1.5	136	1 C17 HUMAN	Q9nrr1 homo sapien
93	6	1.5	136	1 MSC1 PSEFL	O68286 pseudomonas
94	6	1.5	137	1 MSCL PSEAB	P04537 bacterioph
95	6	1.5	137	1 UVS9 BPT4	Q9hsv7 pseudomonas
96	6	1.5	138	1 APEE SYNPI	Q53375 synechococc
97	6	1.5	138	1 EXD1 VIBCH	O52044 vibrio chol
98	6	1.5	138	1 NIKR PYRHO	O58316 pyrococcus
99	6	1.5	138	1 Y337 MYCGE	P47579 mycoplasma
100	6	1.5	140	1 YOR1 CALSR	P40979 caldicellul
101	6	1.5	141	1 V192 FOWPV	Q91541 fowipox vir
102	6	1.5	142	1 TM10 PIG	Q93102 sus scrofa
103	6	1.5	144	1 REV OMVVS	P16903 ovine lenti
104	6	1.5	148	1 GLB3 TYLRE	P13578 tylosrhynch
105	6	1.5	148	1 MSCL PSESM	Q87wb2 pseudomonas
106	6	1.5	150	1 TAA1 VACOC	P20982 vaccinia vi

107	6	1.5	150	1	TAAL_VACCV	P07610	vaccinia vi	180	6	1.5	233	1	H11_GLYSA	P40266	glyptotendi
108	6	1.5	150	1	TAAL_VARV	P33814	variola vir	181	6	1.5	233	1	RNFE_YERPE	Q8264	yersinia pe
109	6	1.5	152	1	NLP_DROME	Q27415	drosophila	182	6	1.5	238	1	RL1_RICPR	Q8263	rickettsia
110	6	1.5	154	1	SDDC_PINSY	P24669	pinus sylve	183	6	1.5	238	1	ZPRO_MOUSE	Q9da39	mus musculus
111	6	1.5	155	1	SSRP_STR33	Q8455	streptococ	184	6	1.5	240	1	COAT_NMV	P15100	narcissus m
112	6	1.5	159	1	BFR_MYCLE	P43315	mycobacteri	185	6	1.5	242	1	PDJ1_NEIMA	Q9trv9	neisseria m
113	6	1.5	159	1	RECK_RALSO	Q8y1v5	ralstonia s	186	6	1.5	242	1	PDJ1_NEIMA	Q9trv9	neisseria m
114	6	1.5	159	1	TPCS_HUMAN	P02585	homo sapien	187	6	1.5	244	1	ADC_CLOAB	P23670	clostridium
115	6	1.5	159	1	TPCS_PIG	P02587	sus scrofa	188	6	1.5	244	1	PRMA_AQUAE	C67870	aquifex aeo
116	6	1.5	159	1	TPCS_RABIT	P02586	oryctolagus	189	6	1.5	245	1	Y125_RICPR	P41087	rickettsia
117	6	1.5	162	1	TPCS_PANES	P02589	rana escul	190	6	1.5	247	1	KADB_APATH	Q8fk35	arabidopsis
118	6	1.5	162	1	Y269_AQUAE	O66626	aquifex aeo	191	6	1.5	248	1	PSB2_THETH	Q8t912	thermoanaer
119	6	1.5	163	1	HMCS_DICDI	P54872	dictyosteli	192	6	1.5	249	1	PSB2_THETH	Q8t912	thermoanaer
120	6	1.5	167	1	REV_VILV	P21280	vigna lenti	193	6	1.5	249	1	PSB2_THETH	Q8t912	thermoanaer
121	6	1.5	167	1	REV_VILV	P21280	vigna lenti	194	6	1.5	250	1	PSB2_THETH	Q8t912	thermoanaer
122	6	1.5	168	1	ATPF_PROMO	P35957	vigna lenti	195	6	1.5	253	1	PSB2_THETH	Q8t912	thermoanaer
123	6	1.5	172	1	CET2_MOUSE	P21904	propionigen	196	6	1.5	253	1	PSB2_THETH	Q8t912	thermoanaer
124	6	1.5	173	1	HSCB_XENNE	Q9rik9	mus musculu	197	6	1.5	255	1	PSB2_THETH	Q8t912	thermoanaer
125	6	1.5	173	1	PR1A_HORVU	P32937	hordeum vul	198	6	1.5	255	1	PSB2_THETH	Q8t912	thermoanaer
126	6	1.5	177	1	APT_DEPIN	P32938	hordeum vul	199	6	1.5	257	1	PSB2_THETH	Q8t912	thermoanaer
127	6	1.5	177	1	APT_DEPIN	P32938	hordeum vul	200	6	1.5	257	1	PSB2_THETH	Q8t912	thermoanaer
128	6	1.5	179	1	YFCP_ECOLI	Q8exn2	leptospira	201	6	1.5	258	1	PSB2_THETH	Q8t912	thermoanaer
129	6	1.5	179	1	YFCP_ECOLI	P76499	escherichia	202	6	1.5	260	1	PSB2_THETH	Q8t912	thermoanaer
130	6	1.5	180	1	Y192_VIBCH	Q9kqv6	vibrio chol	203	6	1.5	262	1	PSB2_THETH	Q8t912	thermoanaer
131	6	1.5	180	1	YK72_VIBVU	P59274	vibrio vuln	204	6	1.5	262	1	PSB2_THETH	Q8t912	thermoanaer
132	6	1.5	181	1	YK69_VIBVU	Q7miz4	vibrio vuln	205	6	1.5	262	1	PSB2_THETH	Q8t912	thermoanaer
133	6	1.5	183	1	AROK_OCEIH	Q8enn6	oceanobacil	206	6	1.5	264	1	PSB2_THETH	Q8t912	thermoanaer
134	6	1.5	183	1	TBP_METJA	Q57930	methanococc	207	6	1.5	264	1	PSB2_THETH	Q8t912	thermoanaer
135	6	1.5	185	1	DUS3_HUMAN	P51452	homo sapien	208	6	1.5	264	1	PSB2_THETH	Q8t912	thermoanaer
136	6	1.5	185	1	DUS3_MOUSE	Q9d7x3	mus musculu	209	6	1.5	266	1	PSB2_THETH	Q8t912	thermoanaer
137	6	1.5	185	1	PSF2_HUMAN	Q9y248	homo sapien	210	6	1.5	266	1	PSB2_THETH	Q8t912	thermoanaer
138	6	1.5	185	1	PSF2_MOUSE	Q9d600	mus musculu	211	6	1.5	266	1	PSB2_THETH	Q8t912	thermoanaer
139	6	1.5	185	1	PSF2_XENLA	Q7zt46	xenopus lae	212	6	1.5	268	1	PSB2_THETH	Q8t912	thermoanaer
140	6	1.5	186	1	YK10_XYLFA	Q9bxb5	xyella fas	213	6	1.5	268	1	PSB2_THETH	Q8t912	thermoanaer
141	6	1.5	186	1	APGB_YEAST	P38316	saccharomyc	214	6	1.5	268	1	PSB2_THETH	Q8t912	thermoanaer
142	6	1.5	189	1	APOD_MOUSE	P59310	mus musculu	215	6	1.5	268	1	PSB2_THETH	Q8t912	thermoanaer
143	6	1.5	190	1	NUSM_ARALI	Q33753	arabacia lix	216	6	1.5	269	1	PSB2_THETH	Q8t912	thermoanaer
144	6	1.5	191	1	YDOT_SCHPO	O13727	schizosacch	217	6	1.5	270	1	PSB2_THETH	Q8t912	thermoanaer
145	6	1.5	191	1	PIC2_AGRU	P29113	agrobacteri	218	6	1.5	274	1	PSB2_THETH	Q8t912	thermoanaer
146	6	1.5	191	1	VISI_CHICK	P22728	gallus gall	219	6	1.5	274	1	PSB2_THETH	Q8t912	thermoanaer
147	6	1.5	193	1	HS72_CANAL	Q45887	candida alb	220	6	1.5	276	1	PSB2_THETH	Q8t912	thermoanaer
148	6	1.5	194	1	PTH_PBSNM	Q888c8	pseudomonas	221	6	1.5	278	1	PSB2_THETH	Q8t912	thermoanaer
149	6	1.5	199	1	PHB1_HUMAN	P31941	homo sapien	222	6	1.5	278	1	PSB2_THETH	Q8t912	thermoanaer
150	6	1.5	199	1	Y104_YEAST	P40447	saccharomyc	223	6	1.5	279	1	PSB2_THETH	Q8t912	thermoanaer
151	6	1.5	201	1	NUGM_CRACA	P48925	cyanidium c	224	6	1.5	281	1	PSB2_THETH	Q8t912	thermoanaer
152	6	1.5	201	1	UL92_HCMVA	P16798	human cytom	225	6	1.5	282	1	PSB2_THETH	Q8t912	thermoanaer
153	6	1.5	205	1	KGUA_HCLPN	P46436	ascaris suu	226	6	1.5	282	1	PSB2_THETH	Q8t912	thermoanaer
154	6	1.5	205	1	KGUA_HCLPN	Q92961	chlamydia p	227	6	1.5	284	1	PSB2_THETH	Q8t912	thermoanaer
155	6	1.5	206	1	PTCA_HUMAN	Q14761	homo sapien	228	6	1.5	286	1	PSB2_THETH	Q8t912	thermoanaer
156	6	1.5	208	1	VG26_BPT4	P13335	bacterioph	229	6	1.5	286	1	PSB2_THETH	Q8t912	thermoanaer
157	6	1.5	209	1	RRM1_ECOLI	P28692	escherichia	230	6	1.5	286	1	PSB2_THETH	Q8t912	thermoanaer
158	6	1.5	210	1	GL34_ARATH	Q9rlt3	arabidopsis	231	6	1.5	286	1	PSB2_THETH	Q8t912	thermoanaer
159	6	1.5	212	1	COAT_PEBV	P14849	pea early b	232	6	1.5	289	1	PSB2_THETH	Q8t912	thermoanaer
160	6	1.5	213	1	KTH2_SULTO	Q970q8	sulfolobus	233	6	1.5	290	1	PSB2_THETH	Q8t912	thermoanaer
161	6	1.5	218	1	MTC2_METMA	P58983	methanosarc	234	6	1.5	293	1	PSB2_THETH	Q8t912	thermoanaer
162	6	1.5	218	1	S125_GALME	O62605	galleria me	235	6	1.5	294	1	PSB2_THETH	Q8t912	thermoanaer
163	6	1.5	219	1	GPX5_PIG	O18994	sus scrofa	236	6	1.5	295	1	PSB2_THETH	Q8t912	thermoanaer
164	6	1.5	220	1	CD28_HUMAN	P10747	homo sapien	237	6	1.5	295	1	PSB2_THETH	Q8t912	thermoanaer
165	6	1.5	221	1	CARE_MYXXA	O06910	myxococcus	238	6	1.5	297	1	PSB2_THETH	Q8t912	thermoanaer
166	6	1.5	221	1	GPX5_HUMAN	O75715	homo sapien	239	6	1.5	297	1	PSB2_THETH	Q8t912	thermoanaer
167	6	1.5	221	1	GPX5_MACFA	P28714	macaca fasc	240	6	1.5	299	1	PSB2_THETH	Q8t912	thermoanaer
168	6	1.5	221	1	GPX5_MOUSE	P59796	homo sapien	241	6	1.5	299	1	PSB2_THETH	Q8t912	thermoanaer
169	6	1.5	222	1	THA6_HUMAN	Q91wr8	mus musculu	242	6	1.5	299	1	PSB2_THETH	Q8t912	thermoanaer
170	6	1.5	223	1	VME1_IBVG	Q8tbb0	homo sapien	243	6	1.5	300	1	PSB2_THETH	Q8t912	thermoanaer
171	6	1.5	223	1	YB43_YEAST	Q910e2	avian infec	244	6	1.5	301	1	PSB2_THETH	Q8t912	thermoanaer
172	6	1.5	224	1	PSMB_METJA	P38304	saccharomyc	245	6	1.5	302	1	PSB2_THETH	Q8t912	thermoanaer
173	6	1.5	224	1	RADC_PASMU	Q58634	methanococ	246	6	1.5	302	1	PSB2_THETH	Q8t912	thermoanaer
174	6	1.5	224	1	RADC_PASMU	P57913	pasteurella	247	6	1.5	303	1	PSB2_THETH	Q8t912	thermoanaer
175	6	1.5	224	1	RNC2_PYRFU	Q8u036	pyrococcus	248	6	1.5	303	1	PSB2_THETH	Q8t912	thermoanaer
176	6	1.5	226	1	RNC_ECOLI	P05797	escherichia	249	6	1.5	305	1	PSB2_THETH	Q8t912	thermoanaer
177	6	1.5	226	1	RNC_SALTI	Q8z4k4	salmonella	250	6	1.5	305	1	PSB2_THETH	Q8t912	thermoanaer
178	6	1.5	226	1	RNC_SALTI	Q56056	salmonella	251	6	1.5	305	1	PSB2_THETH	Q8t912	thermoanaer
179	6	1.5	227	1	PSAF_CHLRE	P12356	chlamydomon	252	6	1.5	306	1	PSB2_THETH	Q8t912	thermoanaer
			232	1	RADC_BACHD	Q9x8h4	bacillus ha								

253	Q83880	treponema p	326	6	1.5	365	1	Y897	ARCFU	Q29365	archaeoglob
254	Q9x9j3	vibrio para	327	6	1.5	366	1	IHA	HUMAN	P05111	homo sapien
255	Q99tj1	staphylococ	328	6	1.5	367	1	V2R	CANFA	P77808	canis famli
256	Q34090	staphylococ	329	6	1.5	370	1	PR82	METUA	Q58889	methanococ
257	Q8nw74	staphylococ	330	6	1.5	371	1	PR82	METUA	Q27092	methanobact
258	Q8cnv8	staphylococ	331	6	1.5	372	1	PR82	METUA	P42811	methanobact
259	Q8thl2	methanosarc	332	6	1.5	372	1	SL7B	HUMAN	Q4768	homo sapien
260	Q8fxj1	brucella su	333	6	1.5	372	1	SL7B	WOUSE	Q8b48	mus musculu
261	Q8cxco	oceanobacil	334	6	1.5	373	1	FLHF	AQUAE	Q67266	aquifex aeo
262	Q8pxk5	methanosarc	335	6	1.5	374	1	RLUD	NEIMA	Q9jvb6	neisseria m
263	Q28487	archaeoglob	336	6	1.5	374	1	RLUD	NEIMA	Q9kdb0	neisseria m
264	Q98h78	rhizobium l	337	6	1.5	375	1	CD14	HUMAN	P08571	homo sapien
265	P40373	schizosacch	338	6	1.5	375	1	IRKF	CAVPO	O70339	cavia porce
266	Q57390	pelobacter	339	6	1.5	375	1	IRKF	HUMAN	O99712	homo sapien
267	Q15620	homo sapien	340	6	1.5	375	1	IRKF	WOUSE	O88932	mus musculu
268	Q95155	canis famli	341	6	1.5	376	1	SI8E	HUMAN	O15466	homo sapien
269	Q9nh18	homo sapien	342	6	1.5	377	1	BEXC	HABIN	P22930	haemophilus
270	Q9vgr8	mus musculu	343	6	1.5	377	1	NADA	CAUCR	Q9a4c4	caulobacter
271	Q9nge7	homo sapien	344	6	1.5	377	1	PROB	MEIRU	Q9z988	meiothermus
272	Q96rd3	homo sapien	345	6	1.5	378	1	CYB	ANOQA	P34844	anopheles g
273	Q8ngf4	homo sapien	346	6	1.5	378	1	CYB	ANOQA	P33501	anopheles q
274	P41883	caenorhabdi	347	6	1.5	379	1	CIT2	ECOLI	P05853	escherichia
275	Q9xae6	oryza sativ	348	6	1.5	381	1	ARRC	MOUSE	Q9eqp6	mus musculu
276	O5941	rhizobium e	349	6	1.5	381	1	C3L1	MOUSE	Q61362	mus musculu
277	P57532	buchnera ap	350	6	1.5	381	1	CYB	ARTSF	Q37713	artemia san
278	Q00834	spinacia ol	351	6	1.5	382	1	SLU7	YEAST	Q02775	saccharomyc
279	O07600	bacillus su	352	6	1.5	383	1	C3L1	HUMAN	P36222	homo sapien
280	Q03874	equine rota	353	6	1.5	384	1	OPGC	SALTI	Q8z027	salmonella
281	Q87j19	clostridium	354	6	1.5	384	1	OPGC	SALTY	Q8zo27	salmonella
282	Q84632	chlamydia c	355	6	1.5	385	1	OPGC	ECOS7	Q8x3i6	escherichia
283	Q7cuas	prochloroco	356	6	1.5	385	1	OPGC	ECOL6	Q8f185	escherichia
284	Q9byul	homo sapien	357	6	1.5	385	1	OPGC	ECOLI	P75920	escherichia
285	P09978	staphylococ	358	6	1.5	387	1	ARGJ	METKA	Q8tx15	m arginine
286	Q913k7	pseudomonas	359	6	1.5	387	1	MDMB	STRMY	Q00718	streptomyce
287	Q73874	brachydanio	360	6	1.5	388	1	ALR	BACHD	Q9kf59	bacillus ha
288	Q8y2l3	rastronia s	361	6	1.5	388	1	ARRC	HUMAN	P36575	homo sapien
289	Q82021	arabidopsis	362	6	1.5	388	1	CARE	STRTH	P21542	streptomyce
290	P53228	saccharomyc	363	6	1.5	389	1	CYB	DICDI	Q37311	dictyosteli
291	P17505	saccharomyc	364	6	1.5	389	1	SIK2	MOUSE	Q8vqg8	mus musculu
292	Q4212	saccharomyc	365	6	1.5	392	1	PATA	BACSU	P16524	bacillus su
293	Q33117	mycobacteri	366	6	1.5	392	1	SYT	AQUAE	O67632	aquifex aeo
294	P23448	bacillus su	367	6	1.5	394	1	FEUC	BACSU	P40411	bacillus su
295	Q12048	saccharomyc	368	6	1.5	394	1	Y129	CHLPN	Q9jtx2	chlamydia p
296	P79949	xenopus lae	369	6	1.5	397	1	CBAC	COMTE	Q42358	comamonas t
297	P05481	bacterioph	370	6	1.5	400	1	FBH1	CUPWR	P49244	cuphea wrig
298	Q9ric0	mus musculu	371	6	1.5	402	1	FBH2	CUPWR	P49243	arabidopsis
299	Q8c131	mus musculu	372	6	1.5	404	1	FABH	ARATH	P41970	homo sapien
300	Q8hmm4	halobacteri	373	6	1.5	407	1	ELK3	HUMAN	P55340	bacillus su
301	O50146	thermus the	374	6	1.5	408	1	EC83	BACSU	P81140	sus scrofa
302	Q8bxc0	homo sapien	375	6	1.5	408	1	GDH	PIG	P27301	escherichia
303	Q15545	homo sapien	376	6	1.5	409	1	MCRD	ECOLI	Q01361	picchia past
304	P06729	homo sapien	377	6	1.5	409	1	PEXC	PICPA	O28631	archaeoglob
305	Q8vw55	oenococcus	378	6	1.5	409	1	SYH	ARCFU	P18161	dictyosteli
306	Q9ny19	homo sapien	379	6	1.5	410	1	KYK2	DICDI	Q32149	bacillus su
307	Q9v4r7	homo sapien	380	6	1.5	412	1	ALIC	BACSU	O32149	bacillus su
308	P36151	saccharomyc	381	6	1.5	412	1	NH64	CABEL	O44960	caenorhabdi
309	Q93747	halobacteri	382	6	1.5	413	1	CYCL	DROME	O61734	drosophila
310	Q56815	xanthobacte	383	6	1.5	414	1	LIP5	YEAST	P32875	saccharomyc
311	P49339	gallus gall	384	6	1.5	415	1	EX7L	MCTU	O53456	mycobacteri
312	P51891	cuturnix co	385	6	1.5	416	1	AROA	ARCFU	O28775	archaeoglob
313	P49256	canis famli	386	6	1.5	417	1	GELS	XENLA	P14885	xenopus lae
314	Q12907	homo sapien	387	6	1.5	417	1	O85E	DROME	P81924	drosophila
315	Q46431	carcopithec	388	6	1.5	419	1	AROA	METTH	O26860	methanobact
316	Q8kg45	chlorobium	389	6	1.5	419	1	HASA	STRPY	O54865	streptococ
317	P88336	rhizobium m	390	6	1.5	419	1	SEP2	DROME	P54359	drosophila
318	Q12926	homo sapien	391	6	1.5	420	1	PROA	PASMU	Q9cm98	pasteurella
319	Q60899	mus musculu	392	6	1.5	421	1	MUAI	CLOPE	O21191	streptococ
320	Q9ugm6	homo sapien	393	6	1.5	422	1	ENO	STRTR	O52156	bacillus su
321	P73341	synechocyst	394	6	1.5	422	1	YUO	BACSU	O84591	chlamydia t
322	O43427	homo sapien	395	6	1.5	424	1	ENO	CHLTR	P49461	odontella s
323	P24827	pseudorabie	396	6	1.5	425	1	SEGY	ODOSI	Q9ruv5	deinococcus
324	Q9r024	cavia porce	397	6	1.5	425	1	SY8	DEIRA	Q9wzf8	thermocoga
325	O48910	oryctolagus	398	6	1.5	425	1	TIG	THEMA		

399	1	1.5	426	1	SYH_SULTO	Q975u9 sulfolobus
400	1	1.5	427	1	TCO2 RAT	Q9r0d6 rattus norv
401	1	1.5	428	1	AROA_LISIN	Q92a85 listeria m
402	1	1.5	428	1	AROA_LISIN	Q9v5v0 listeria m
403	1	1.5	428	1	LAAX_XENLA	P28048 xenopus lae
404	1	1.5	429	1	HL5X_METJA	Q58851 methanococ
405	1	1.5	429	1	MUA2_BACSU	P19670 bacillus su
406	1	1.5	430	1	AMPP_HAEIN	P44881 haemophilus
407	1	1.5	430	1	YJCF_ECOLI	P32704 escherichia
408	1	1.5	431	1	PD22_DROME	Q9w088 drosophila
409	1	1.5	431	1	PKNA_MYCTU	P1585 mycobacteri
410	1	1.5	432	1	ACDB_HUMAN	P45954 h acyl-coa
411	1	1.5	432	1	ENO_STRMU	Q8dtr9 streptococ
412	1	1.5	432	1	MURD_FUSNN	Q8rdq1 streptococ
413	1	1.5	433	1	ENOA_LACIA	Q8che7 lactococ
414	1	1.5	433	1	OADB_VIBCH	Q9ktu5 vibrio chol
415	1	1.5	433	1	TIG_CHLMU	Q9pl19 chlamydia m
416	1	1.5	434	1	ENO_SKRIT	Q9xds7 streptococ
417	1	1.5	434	1	ENO_STRPN	Q97qs2 streptococ
418	1	1.5	434	1	ENO_STRPY	P82479 streptococ
419	1	1.5	434	1	ERFB_ARATH	Q8p80 streptococ
420	1	1.5	434	1	SEP6_HUMAN	Q9lpv8 arabidopsis
421	1	1.5	434	1	SEP6_MOUSE	Q14141 homo sapien
422	1	1.5	434	1	YRL4_CABEL	Q9rit4 mus musculu
423	1	1.5	434	1	ENO_STR3	Q09413 caenorhabdi
424	1	1.5	435	1	ERFC_ARATH	Q8e690 streptococ
425	1	1.5	435	1	SCB1_CABEL	P35614 arabidopsis
426	1	1.5	435	1	ERF1_BLEAM	P53588 caenorhabdi
427	1	1.5	436	1	ARGA_PASMU	Q9bmm3 blepharisma
428	1	1.5	440	1	ENO1_CANAL	Q9cmj6 pasteurella
429	1	1.5	441	1	SECV_HAEIN	P30575 candida alb
430	1	1.5	441	1	TOXE_COCCA	P43804 haemophilus
431	1	1.5	441	1	CEM1_YEAST	Q74205 cochlidiobol
432	1	1.5	442	1	GNT2_RAT	P39525 saccharomyc
433	1	1.5	442	1	TIG_CHLPN	Q09326 r alpha-1,6
434	1	1.5	442	1	TIG_CHLTP	Q92758 chlamydia p
435	1	1.5	442	1	CEGH_XANMA	O84713 chlamydia t
436	1	1.5	443	1	PEPO_ECOLI	P37126 xanthomonas
437	1	1.5	443	1	ERFI_OXYTR	P21165 escherichia
438	1	1.5	445	1	ERFI_STYMT	Q9bmx3 oxytricha t
439	1	1.5	445	1	MCRB_METJA	Q9bmm1 stylyonchia
440	1	1.5	447	1	ENGA_MYCPN	Q58252 methanococ
441	1	1.5	449	1	SORD_HUMAN	P75309 mycoplasma
442	1	1.5	450	1	Y600_TREPA	Q9y6n5 homo sapien
443	1	1.5	450	1	HS83_LEIDO	O83609 treponema p
444	1	1.5	451	1	VATB_CHICK	P27890 leishmania
445	1	1.5	453	1	HYEP_RABIT	P49712 gallus gall
446	1	1.5	455	1	FURL_ARCFU	P04068 oryctolagus
447	1	1.5	456	1	ARLY_HELMO	O29388 archaeglob
448	1	1.5	458	1	EFLA_AEXAD	P41745 axulla aden
449	1	1.5	459	1	DPD3_MOUSE	Q89c45 hellobacill
450	1	1.5	462	1	SELA_YERPE	Q9eq28 mus musculu
451	1	1.5	463	1	GLGA_AQUAE	Q8z9y1 yersinia pe
452	1	1.5	463	1	CHT1_HUMAN	O66935 aquifex aeo
453	1	1.5	466	1	DPD2_HUMAN	Q13231 homo sapien
454	1	1.5	466	1	NORB_PSEAE	Q15054 homo sapien
455	1	1.5	466	1	VP19_HSV2G	Q59647 pseudomonas
456	1	1.5	466	1	6PGD_BACLI	P22486 herpes simp
457	1	1.5	467	1	LEU2_BORBP	P89461 herpes simp
458	1	1.5	467	1	LEU2_BORBP	P52207 bacillus li
459	1	1.5	467	1	LEU2_BORBP	Q7wk96 bordetella
460	1	1.5	467	1	PCOI_MOUSE	Q7v775 bordetella
461	1	1.5	467	1	PCOI_MOUSE	Q9yc12 aeropyrum p
462	1	1.5	468	1	TNAA_XENLA	Q61398 mus musculu
463	1	1.5	472	1	TNAA_XENLA	P19102 xenopus lae
464	1	1.5	473	1	TNAA_VIBVU	Q8d5q4 vibrio vuln
465	1	1.5	474	1	NOA1_RAT	Q80wa4 rattus norv
466	1	1.5	474	1	FACI_HUMAN	Q75844 homo sapien
467	1	1.5	475	1	GAB1_CLOAB	Q97f58 clostridium
468	1	1.5	476	1	YS5A_CABEL	Q09663 caenorhabdi
469	1	1.5	477	1	AMT_MYCTU	Q10968 mycobacteri
470	1	1.5	477	1	LE21_BRAJA	Q89x98 bradyrhizob
471	1	1.5	477	1		

ALIGNMENTS

RESULT 1

ID	PVAA_STRP3	STANDARD;	PRT;	199 AA.
AC	Q8K7H6;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Pneumococcal vaccine antigen A homolog.			
GN	PVAA OR SPVX3 0805 OR SP81004.			
OS	Streptococcus pyogenes (serotype M3).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=198466;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MGAS315 / Serotype M3;			
RX	MEDLINE=22133808; PubMed=12122206;			
RA	Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,			
RA	Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,			
RA	Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,			
RA	Schlievert P.M., Musser J.M.;			
RT	"Genome sequence of a serotype M3 strain of group A Streptococcus:			
RT	phage-encoded toxins, the high-virulence phenotype, and clone			
RT	emergence."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SSI-1 / Serotype M3;			
RX	MEDLINE=22683278; PubMed=12799345;			
RA	Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,			
RA	Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,			
RT	Hayashi H., Hattori M., Hamada S.;			
RT	"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a			
RT	large-scale genomic rearrangement in invasive strains and new insights			
RT	into phage evolution."			
RL	Genome Res. 13:1042-1055(2003).			
CC	-1- SUBCELLULAR LOCATION: Cell surface (By similarity).			
CC	-----			
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-----
DR EMBL; AF014152; AAM79412.1; -
DR EMBL; AF005144; BAC64039.1; -
KW Antigen; Complete proteome.
SQ SEQUENCE 199 AA; 22101 MW; 3658DDF864AC0F7C CRC64;

Query Match 2.0%; Score 8; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 KNSITDSQ 49
DB 79 KNSITDSQ 86

RESULT 2
PVA STRP8
ID PVA STRP8 STANDARD; PRT; 199 AA.
AC Q8PI20;
DT 28-FEB-2003 (Rel. 41, Created)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE Pneumococcal vaccine antigen A homolog.
GN PVA OR SPV18 1107.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
CC -!- SUBCELLULAR LOCATION: Cell surface (By similarity).
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-----
DR EMBL; AE010036; AAL97729.1; -
DR Antigen; Complete proteome.
SQ SEQUENCE 199 AA; 22071 MW; 8258DD5B96C12A1 CRC64;

Query Match 2.0%; Score 8; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 KNSITDSQ 49
DB 79 KNSITDSQ 86

RESULT 3
PVA STRP9
ID PVA STRP9 STANDARD; PRT; 199 AA.
AC Q99ZN9;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pneumococcal vaccine antigen A homolog.
GN PVA OR SP1147.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
CC -!- SUBCELLULAR LOCATION: Cell surface (By similarity).
-----
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-----
DR EMBL; AE006556; AAK34019.1; -
KW Antigen; Complete proteome.
SQ SEQUENCE 199 AA; 22072 MW; B455653B96C1A89 CRC64;

Query Match 2.0%; Score 8; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 KNSITDSQ 49
DB 79 KNSITDSQ 86

RESULT 4
DNAK LISIN
ID DNAK LISIN STANDARD; PRT; 612 AA.
AC Q92BN8;
DT 28-FEB-2003 (Rel. 41, Created)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70).
GN DNAK OR LIN1510.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Cherouani P., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauguet O.,
RA Entian K.-D., Feihl H., Garcia-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Kunst F., Kurapkat G.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunz F., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstedt G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852 (2001).
CC -!- FUNCTION: Acts as a chaperone (By similarity).

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CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC -----
DR EMBL; AL596168; CAC96741.1; -
DR PIR; AE1621; AE1621.
DR Listlist; L1N01510; -
DR HAMAP; MF 00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation;
KW Complete proteome.
FT INIT MET 0 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 612 AA; 65997 MW; E38C2CE223B8E08 CRC64;

Query Match 2.0%; Score 8; DB 1; Length 612;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEIKM 397
Db 477 TDEIEIKM 484
|||||

RESULT 5
DNAME LISMO STANDARD; PRT; 612 AA.
AC Q955A4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70).
GN DNAME OR LMO1473.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10403S;
RX MEDLINE=20163771; PubMed=10701836;
RA Hanawa T., Kai M., Kamiya S., Yamamoto T.;
RT "Cloning, sequencing, and transcriptional analysis of the dnaK heat
RT shock operon of Listeria monocytogenes.";
RL Cell Stress Chaperones 5:21-29(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Deboux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Enian K.-D., Feih H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjati H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

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RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC -----
DR EMBL; AB023064; BAA83789.1; -
DR EMBL; AL591979; CAC939551.1; -
DR PIR; A11258; A11258.
DR PIR; T43738; T43738.
DR HSP; P04475; IDG4.
DR Listlist; LMO01473; -
DR HAMAP; MF 00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation;
KW Complete proteome.
FT INIT MET 0 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 243 243 S->F (IN REF. 1).
SQ SEQUENCE 612 AA; 66012 MW; 4D6D2120C238FC4 CRC64;

Query Match 2.0%; Score 8; DB 1; Length 612;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEIKM 397
Db 477 TDEIEIKM 484
|||||

RESULT 6
DNAME LISMO STANDARD; PRT; 1138 AA.
AC Q955A4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE PDZ domain containing guanine nucleotide exchange factor 1 (PDZ-GEF1
DE (Fragment)).
GN PDZGEF1 OR KIAA0313.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22353125; PubMed=12465718;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 9:179-188(2002).
CC -!- FUNCTION: Guanine nucleotide exchange factor (GEF) for Rap1 and
CC Rap2 GTPases (By similarity).
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 1 Ras-associating domain.

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CC -|- SIMILARITY: Contains 1 Ras-GEF domain.
CC -----
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CC -----
CC EMBL; AB093228; BAC41412.1; -.
CC PIR; PT0615; PT0686.
CC MGI; 2659071; Pd2gef1.
CC InterPro; IPR001478; PDZ.
CC InterPro; IPR000159; RA_domain.
CC InterPro; IPR008937; Ras_GEF.
CC InterPro; IPR001895; RasGEF_CDC25.
CC Pfam; PF00595; PDZ; 1.
CC Pfam; PF00788; RA; 1.
CC Pfam; PF00617; RasGEF; 1.
CC SMART; SM00228; PDZ; 1.
CC SMART; SM00314; RA; 1.
CC SMART; SM00147; RasGEF; 1.
CC PROSITE; PS0106; PDZ; 1.
CC PROSITE; PS0200; RA; 1.
CC PROSITE; PS0009; RasGEF CAT; 1.
KW Guanine-nucleotide releasing factor.
FT NON_TER 1
FT DOMAIN 27 112 PDZ-ASSOCIATING.
FT DOMAIN 248 334 RAS-ASSOCIATING.
FT DOMAIN 359 586 RAS-GEF.
FT DOMAIN 749 807 SER-RICH.
FT DOMAIN 1040 1121 PRO-RICH.
FT SEQUENCE 1138 AA; 548D4D6EBF364CB1 CRC64;
SQ
Query Match 2.0%; Score 8; DB 1; Length 1138;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 QALKKILS 90
Db 723 QALKKILS 730
-----
RESULT 7
KF4A XENLA
ID KF4A XENLA STANDARD; PRT; 1226 AA.
AC Q91784; O9PSI0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chromosome-associated kinesin KLP1 (Chromokinesin).
GN KLP1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
SPECIFICITY.
RC TISSUE=Oocyte;
RX MEDLINE=95236444; PubMed=7720067;
RA Vernos I., Raats J., Hirano T., Heasman J., Karsenti E., Wylie C.;
RT "Xklp1, a chromosomal Xenopus kinesin-like protein essential for
RT spindle organization and chromosome positioning.";
RL Cell 81:117-127(1995).
RN [2]
RP SEQUENCE OF 9-338 FROM N.A.
RX MEDLINE=93246065; PubMed=8482413;
RA Vernos I., Heasman J., Wylie C.;
RT "Multiple kinesin-like transcripts in Xenopus oocytes.";

```

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RL Dev. Biol. 157:232-239(1993).
CC -|- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOLAR
CC SPINDLE STABILIZATION. Nuclear. Associated with mitotic
CC SUBCELLULAR LOCATION: Nuclear.
CC -|- TISSUE SPECIFICITY: Expressed in oocytes, eggs, testes and
CC brain.
CC -|- SIMILARITY: Belongs to the kinesin-like protein family.
CC Chromokinesin subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X82012; CAAS7539.1; -.
CC PIR; I51617; I51617.
CC HSP; P17119; 3KAR.
CC InterPro; IPR001752; kinesin_motor.
CC Pfam; PF00225; kinesin; 1.
CC PRINTS; PR00380; KINESINHEAVY.
CC SMART; SM00129; KISC; 1.
CC PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
CC PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.
KW Motor protein; Microtubule; ATP-binding; DNA-binding;
KW Nuclear protein; Coiled coil.
FT DOMAIN 1 350 KINESIN-MOTOR.
FT DOMAIN 351 1006 COILED COIL (BY SIMILARITY).
FT DOMAIN 1007 1226 GLOBULAR.
FT NP_BIND 87 94 ATP (POTENTIAL).
FT CONFLICT 163 163 I -> L (IN REF. 2).
FT SEQUENCE 1226 AA; 138923 MW; 7F0275FCF3316697 CRC64;
SQ
Query Match 2.0%; Score 8; DB 1; Length 1226;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 391 DEEIEKMK 398
Db 974 DEEIEKMK 981
-----
RESULT 8
PGF1 HUMAN
ID PGF1 HUMAN STANDARD; PRT; 1499 AA.
AC Q9Y4G8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE PDZ domain containing guanine nucleotide exchange factor 1 (PDZ-GEF1)
DE (RA-GEF).
GN PDZGEF1 OR KIAA0313.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97349984; PubMed=9205841;
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 4:141-150(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=20076489; PubMed=10608883;
RA de Rooij J., Boenink N.M., van Triest M., Cool R.H., Wittinghofer A.,

```

RA Bos J.L.;
RT "PDZ-GFP1, a guanine nucleotide exchange factor specific for Rap1 and
RT Rap2";
RL J. Biol. Chem. 274:38125-38130(1999).
RN [3]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=20519575; PubMed=1034404;
RA Rebbun J.F., Castro A.F., Quilliam L.A.;
RT "Identification of guanine nucleotide exchange factors (GEFs) for the
RT Rap1 GTPase. Regulation of MR-GEF by M-Ras-GTP interaction.";
RL J. Biol. Chem. 275:34901-34908(2000).
CC -1- FUNCTION: Guanine nucleotide exchange factor (GEF) for Rap1A and
CC -1- Rap2B GTPases. It does not interact with cAMP or cGMP.
CC -1- TISSUE SPECIFICITY: Highest expression levels in brain. Lower
CC expression levels in heart, kidney, lung, and placenta.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -1- SIMILARITY: Contains 1 N-terminal Ras-GEF domain.
CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -1- SIMILARITY: Contains 1 Ras-associating domain.
CC -1- SIMILARITY: Contains 1 Ras-GEF domain.
CC
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CC
CC EMBL; AB02311; BAA20772.1; -
CC GenBank; HGNC:16854; PDZGEF1.
CC InterPro; IPR000595; CNMP_binding.
CC InterPro; IPR001478; PDZ_1.
CC InterPro; IPR000159; RA_domain.
CC InterPro; IPR008937; Ras_GEF.
CC InterPro; IPR000651; RasGEFN.
CC InterPro; IPR001895; RasGEF_CDC25.
CC Pfam; PF00027; CNMP_binding; 1.
CC Pfam; PF00595; PDZ; 1.
CC Pfam; PF00788; RA; 1.
CC Pfam; PF00617; RasGEF; 1.
CC Pfam; PF00618; RasGEFN; 1.
CC SMART; SM00100; CNMP; 1.
CC SMART; SM00228; PDZ; 1.
CC SMART; SM00314; RA; 1.
CC SMART; SM00147; RasGEF; 1.
CC SMART; SM00229; RasGEFN; 1.
CC PROSITE; PS50042; CNMP_BINDING_3; 1.
CC PROSITE; PS50106; PDZ; 1.
CC PROSITE; PS50200; RA; 1.
CC PROSITE; PS50009; RasGEF_CAT; 1.
CC PROSITE; PS50212; RasGEF_NTER; 1.
CC Guanine-nucleotide releasing factor.
KW NP_BIND 135 254 CNMP.
FT DOMAIN 267 380 N-TERMINAL RAS-GEF.
FT DOMAIN 385 470 PDZ.
FT DOMAIN 606 692 RAS-ASSOCIATING.
FT DOMAIN 717 944 RAS-GEF.
FT DOMAIN 1108 1166 SER-RICH.
SQ SEQUENCE 1499 AA; 167415 MW; 1909E8A12637E001 CRC64;

Query Match 2.08; Score 8; DB 1; Length 1499;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QALKKILS 90
DB 1082 QALKKILS 1089

RESULT 9
SUGES_PROVU STANDARD; PRT; 104 AA.
ID SUGES_PROVU

P20928;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUGES protein homolog.
GN SUGES.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88004470; PubMed=3308458;
RA Cole S.T.;
RT "Nucleotide sequence and comparative analysis of the frd operon
RT encoding the fumarate reductase of Proteus vulgaris. Extensive
RT sequence divergence of the membrane anchors and absence of an
RT frd-linked ampC cephalosporinase gene.";
RL Eur. J. Biochem. 167:481-488(1987).
CC -1- FUNCTION: COULD ACT AS A CHAPERONE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the small multidrug resistance (SMR)
CC protein family.
CC
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CC
CC EMBL; X06151; CAA29512.1; -
CC PIR; S00120; S00120.
CC InterPro; IPR000390; Smr.
CC Pfam; PF00893; Multi_Drug_Res; 1.
CC Chaperone; Transmembrane.
KW TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 29 49 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 84 104 POTENTIAL.
SQ SEQUENCE 104 AA; 11014 MW; 1A1F4AC9C7A94955 CRC64;

Query Match 1.78; Score 7; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 LTPSIIT 141
DB 29 LTPSIIT 35

RESULT 10
SUGES_CITFR STANDARD; PRT; 105 AA.
AC O69279;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUGES protein homolog.
GN SUGES.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=OS60;
RX MEDLINE=98344100; PubMed=9677290;
RA Bishop R.E., Leski B.K., Hodges R.S., Kay C.M., Weiner J.H.;
RT "The entericidin locus of Escherichia coli and its implications for
RT programmed bacterial cell death.";
RT J. Mol. Biol. 280:583-596(1998).
RL

CC -!- FUNCTION: COULD ACT AS A CHAPERONE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the small multidrug resistance (SMR)
CC protein family.
CC -----
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CC -----
CC EMBL; U2127; AAC46457.1; -
CC InterPro; IPR000390; Smr.
CC Pfam; PF00893; Multi Drug Res; 1.
CC Chapterone; Transmembrane; Transport.
CC TRANSMEM 1 21 POTENTIAL.
CC TRANSMEM 29 49 POTENTIAL.
CC TRANSMEM 58 78 POTENTIAL.
CC TRANSMEM 82 102 POTENTIAL.
CC SEQUENCE 105 AA; 10897 MW; 62DA129ADA86E765 CRC64;
CC -----
CC Query Match 1.7%; Score 7; DB 1; Length 105;
CC Best Local Similarity 100.0%; Pred. No. 17;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 135 LTPSIIT 141
CC Db 29 LTPSIIT 35
CC -----
CC RESULT 11
CC PTSN_BRAJA STANDARD; PRT; 153 AA.
CC ID PTSN_BRAJA
CC AC P30335;
CC DT 01-APR-1993 (Rel. 25, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Nitrogen regulatory IIA protein (EC 2.7.1.69) (Enzyme IIA-NTR)
CC DE (Phosphotransferase enzyme II, A component).
CC GN PTSN OR BLR0725.
CC OS Bradyrhizobium japonicum.
CC OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC OC Bradyrhizobiaceae; Bradyrhizobium.
CC OX NCBI_TaxID=375;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=USDA 110;
CC RX MEDLINE=22484998; PubMed=12597275;
CC RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
CC RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
CC RA Kohara M., Matsumoto M., Shampo S., Tsuruoka H., Wada T., Yamada M.,
CC RA Tabata S.;
CC RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
CC RT Bradyrhizobium japonicum USDA110."
CC RL DNA Res. 9:189-197(2002).
CC RN [2]
CC RP SEQUENCE OF 1-90 FROM N.A.
CC RC STRAIN=USDA 110sep4;
CC RX MEDLINE=91123185; PubMed=1991712;
CC RA Kullik I., Fritzsche S., Knobel H., Sanjuan J., Hennecke H.,
CC RA Fischer H.-M.;
CC RT "Bradyrhizobium japonicum has two differentially regulated,
CC RT functional homologs of the sigma 54 gene (rpoN).";
CC RL J. Bacteriol. 173:1125-1138 (1991).
CC CC -!- FUNCTION: Seems to have a role in linking carbon and nitrogen
CC assimilation (by similarity).
CC CC -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
CC histidine + sugar phosphate.
CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC -!- SIMILARITY: BELONGS TO THE PTS IIA FAMILY.
CC -----

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CC -----
CC EMBL; AP005937; BAC45990.1; -
CC EMBL; M59243; AAA26243.1; -
CC PUR; D38179; D38179.
CC HSP; P31222; IAGJ.
CC InterPro; IPR002178; PTS_EIIA_2.
CC InterPro; IPR006320; PtsN_nitro_regn.
CC Pfam; PF00359; PTS_EIIA_2; 1.
CC ProDom; PD001689; PTS_EIIA_2; 1.
CC TIGRFAMs; TIGR01419; nitro_reg_IIA; 1.
CC PROSITE; PS00372; PTS_EIIA_2; 1.
CC KW Phosphotransferase system; Transferase; Phosphorylation;
CC Complete proteome.
CC FT MOD_RES 66 66 PHOSPHORYLATION (BY SIMILARITY).
CC SQ SEQUENCE 153 AA; 16455 MW; 9B52C7F34E2D491A CRC64;
CC -----
CC Query Match 1.7%; Score 7; DB 1; Length 153;
CC Best Local Similarity 100.0%; Pred. No. 24;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 129 DLVFLLL 135
CC Db 97 DLVFLLL 103
CC -----
CC RESULT 12
CC YITZF_BACSU STANDARD; PRT; 157 AA.
CC ID YITZF_BACSU
CC AC O32068;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Hypothetical pseudouridine synthase YtzF (EC 4.2.1.70)
CC DE (Pseudouridylylase)
CC GN YITZF OR BSU30030.
CC OS Bacillus subtilis.
CC OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC OX NCBI_TaxID=1423;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=168;
CC RX MEDLINE=98044033; PubMed=9384377;
CC RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
CC RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
CC RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
CC RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
CC RA Choi S.K., Codari J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
CC RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
CC RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
CC RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi E.J., Grandi G.,
CC RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Galletti N.,
CC RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
CC RA Hilbert H., Holsappel S., Hosono S., Hullo M.P., Itaya M., Jones L.,
CC RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
CC RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
CC RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
CC RA Lee S.M., Levine A., Liu H., Masuda S., Maestl D., Nakai S., Noback M.,
CC RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Park S.H.,
CC RA Noone D., O'Reilly M., Ogawa K., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
CC RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
CC RA Prasecan B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
CC RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
CC RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
CC RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
CC RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
CC RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,

RA Toato V., Uchiyama S., Vanderbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambit R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT *subtilis*";
RL Nature 390:249-256 (1997).
CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate -> pseudouridine
CC -!- 5-phosphate + H(2)O.
CC -!- SIMILARITY: Belongs to the pseudouridine synthase rsuA family.
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CC -----
DR EMBL; Z99119; CAB14981.1; -;
DR PIR; H70004; H70004.
DR Subtilist; BG13940; YtzF.
DR InterPro; IPR006145; Pseudou synth.
DR InterPro; IPR000748; Psi_synth_RSU.
DR Pfam; PF00849; Pseudou synth_2; 1.
DR TIGRFAMs; TIGR00093; TIGR00093; 1.
DR PROSITE; PS01149; Psi_RSU; 1.
KW Hypothetical protein; Lyase; Complete proteome.
FT ACT SITE 21 21 BY SIMILARITY.
SQ SEQUENCE 157 AA; 17695 MW; D378BFA41E89DCE1 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 24; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
Qy 28 DTGFFLL 34
Db 23 DTGFFLL 29

RESULT 13
YG6 YEAST
ID YG6 YEAST STANDARD; PRT; 165 AA.
AC P53095;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 18.1 kDa protein in MDS3-GCN1 intergenic region.
GN YGL198W OR G1315.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=97197971; PubMed=9046087;
RA Coglievina M., Kilma R., Bertani I., Delneri D., Zaccaria P.,
RA Bruschi C.V.;
RT "Sequencing of a 40.5 kb fragment located on the left arm of
RT chromosome VII from *Saccharomyces cerevisiae*.";
RL Yeast 13:55-64 (1997).
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 148.
CC -----
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CC -----

DR EMBL; Z72718; CAA96908.1; -;
DR EMBL; X91837; CAA62948.1; ALT_FRAME.
DR PIR; S64213; S64213.
DR Germline; 141244; -;
DR SGD; S0003164; YGL196W.
KW Hypothetical protein.
SQ SEQUENCE 165 AA; 18101 MW; 305A400B68B7F080 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 LSGFVLG 16
Db 84 LSGFVLG 90

RESULT 14
VB07 VACC
ID VB07 VACC STANDARD; PRT; 182 AA.
AC P21003;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein 57 precursor.
GN B7R.
OS Vaccinia virus (strain WR), and
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254; 10249;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WR;
RX MEDLINE=91259063; PubMed=2045793;
RA Smith G.L., Chan Y.S., Howard S.T.;
RT "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
RT the right inverted terminal repeat.";
RL J. Gen. Virol. 72:1349-1376 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WR;
RX MEDLINE=91111982; PubMed=1846491;
RA Howard S.T., Chan Y.S., Smith G.L.;
RT "Vaccinia virus homologues of the Shope fibroma virus inverted
RT terminal repeat proteins and a discontinuous ORF related to the tumor
RT necrosis factor receptor family.";
RL Virology 180:633-647 (1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Copenhagen;
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paolletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266 (1990).
RN [4]
RP COMPLETE GENOME.
RC STRAIN=Copenhagen;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paolletti E.;
RT Appendix to 'The complete DNA sequence of vaccinia virus';
RL Virology 179:517-563 (1990).
CC -----
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CC -----
DR EMBL; D11079; BAA01837.1; -;

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DR EMBL; M58056; AAA47966.1; -
DR EMBL; M35027; AAA48204.1; -
DR PIR; J01801; J01801
DR PIRSF; PIRSF003778; VAC_C81; 1.
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 182 PROTEIN B7.
SQ SEQUENCE 182 AA; 21312 MW; E3086489CCF3557B CRC64;

Query Match 1.7%; Score 7; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
Db 62 SIITESC 68

RESULT 15
ID Y458 METJA STANDARD; PRT; 216 AA.
AC Q57900;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0458.
GN MJ0458.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;

SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sulton G.G., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sulton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Keriavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii";
RL Science 273:1058-1073 (1996).

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CC -----
DR EMBL; U67496; AAB98446.1; -
DR PIR; B64357; B64357.
DR TIGR; MJ0458; -.
DR InterPro; IPR001048; Aa_kinase.
DR Pfam; PF00696; aakinas; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 216 AA; 24080 MW; 37856E333F3D2A76 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 216;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
Db 89 LKREIEK 95

RESULT 16
GPXS CANFA STANDARD; PRT; 221 AA.
AC O46607;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Epididymal secretory glutathione peroxidase precursor (EC 1.11.1.9)
DE Epididymis-specific glutathione peroxidase-like protein (EGLP).
GN GPX5.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;

[1]
SEQUENCE FROM N.A.
TISSUE=epididymis;
MEDLINE=98304457; PubMed=9640275;
RA Beiglböck A., Pera I., Ellerböck K., Kirchhoff C.;
RT "Dog epididymis-specific mRNA encoding secretory glutathione
RT peroxidase-like protein.";
RL J. Reprod. Fert. 112:357-367 (1998).
CC -!- FUNCTION: Protects cells and enzymes from oxidative damage, by
CC catalyzing the reduction of hydrogen peroxide, lipid peroxides and
CC organic hydroperoxide, by glutathione. May constitute a
CC glutathione peroxidase-like protective system against peroxide
CC damage in sperm membrane lipids.
CC -!- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Epididymis.
CC -!- SIMILARITY: Belongs to the glutathione peroxidase family.

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CC -----
DR EMBL; AF045195; AAC02550.1; -
DR HSPF; P00435; IGP1.
DR InterPro; IPR000889; Glut_peroxidase.
DR Pfam; PF00255; GSHPx; 1.
DR PRINTS; PR01011; GLUTPROXDASE.
DR PROSITE; PS00460; GLUTATHIONE PEROXID 1; FALSE_NEG.
DR PROSITE; PS00763; GLUTATHIONE PEROXID 2; 1.
KW Oxidoreductase; Peroxidase; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 221 EPIDIDYMAL SECRETORY GLUTATHIONE
FT ACT SITE 73 73 BY SIMILARITY.
SQ SEQUENCE 221 AA; 25338 MW; C90EF0F0B88C9ACF CRC64;

Query Match 1.7%; Score 7; DB 1; Length 221;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELK 227
Db 84 SLOEELK 90

RESULT 17
MPGP PYRFU STANDARD; PRT; 242 AA.
AC Q8U381;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mannosyl-3-phosphoglycerate phosphatase (EC 3.1.3.70) (MPGP).
GN MNGB OR PF0590.
OS Pyrococcus furiosus.
```



```
CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]_
SEQUENCE FROM N.A.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Hydrolyzes mannoseyl-3-phosphoglycerate (MPG) to form the
CC osmolyte mannoseylglycerate (MG) (By similarity).
CC -!- CATALYTIC ACTIVITY: 2(alpha-D-mannosyl)-3-phosphoglycerate + H(2)O
CC = 2(alpha-D-mannosyl)-D-glycerate + phosphate.
CC -!- PATHWAY: Biosynthesis of alpha-mannoseylglycerate from GDP-mannose;
CC second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the HAD superfamily. MFGP family.
CC
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CC
CC EMBL; AE010181; AAL80714.1; -.
CC HAMAP; MF_00617; 1.
CC InterPro; IPR006379; HAD_SF_IIB.
CC DR TIGRFAMs; TIGR01486; HAD-SF-IIB-YedP; 1.
CC DR TIGRFAMs; TIGR01484; HAD-SF-IIB; 1.
CC KW Hydrolase; Complete proteome.
CC SEQUENCE 242 AA; 28022 MW; 133DE5E84F80AC02 CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 242;
CC Best Local Similarity 100.0%; Pred. No. 35;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 390 TDEIEK 396
CC DB 119 TDEIEK 125
CC
CC RESULT 18
CC SURE_NITEU STANDARD; PRT; 247 AA.
CC AC Q82V79;
CC DT 15-MAR-2004 (Rel. 43, Created)
CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
CC DE Acid phosphatase sure (EC 3.1.3.2).
CC GN SURE OR NE0950.
CC OS Nitrosomonas europaea.
CC OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
CC OC Nitrosomonadaceae; Nitrosomonas.
CC OX NCBI_TaxID=915;
CC RN [1]_
CC SEQUENCE FROM N.A.
CC RC STRAIN=ATCC 19718 / IFO 14298;
CC RX MEDLINE=22596410; PubMed=12700255;
CC RA Chain P., Lamerdin J.E., Larizer F.W., Regala M., Lao V., Land M.,
CC Hauser L., Hooper A.B., Klorz M.G., Norton J., Sayavedra-Soto L.A.,
CC Arciero D.M., Hommes N.G., Whitaker M.M., Arp D.J.;
CC RT "Complete genome sequence of the ammonia-oxidizing bacterium and
CC obligate chemolithoautotroph Nitrosomonas europaea.";
CC RL J. Bacteriol. 185:2759-2773(2003).
CC CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- COPACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the sure acid phosphatase family.
CC
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CC
CC EMBL; BX321859; CAD84861.1; -.
CC HAMAP; MF_00060; 1.
CC InterPro; IPR002828; SURE.
CC DR Pfam; PF01975; SURE; 1.
CC DR ProDom; PD005378; SURE; 1.
CC DR TIGRFAMs; TIGR00087; sure; 1.
CC KW Hydrolase; Magnesium; Complete proteome.
CC FT ACT_SITE 123 123 POTENTIAL.
CC FT METAL 8 8 MAGNESIUM (BY SIMILARITY).
CC FT METAL 9 9 MAGNESIUM (BY SIMILARITY).
CC FT METAL 39 39 MAGNESIUM (BY SIMILARITY).
CC FT METAL 91 91 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 247 AA; 26851 MW; 173C0E7104B384D1 CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 247;
CC Best Local Similarity 100.0%; Pred. No. 36;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 29 TEGFLG 35
CC DB 110 TEGFLG 116
CC
CC RESULT 19
CC Y727_METTH STANDARD; PRT; 256 AA.
CC AC O26823;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Hypothetical UPF0280 protein MTH727.
CC GN MTH727.
CC OS Methanobacterium thermoautotrophicum.
CC OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
CC OC Methanobacteriaceae; Methanothermobacter.
CC OX NCBI_TaxID=187420;
CC RN [1]_
CC SEQUENCE FROM N.A.
CC RC STRAIN=Delta H;
CC RX MEDLINE=98037514; PubMed=9371463;
CC RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
CC Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
CC Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
CC Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
CC Jiwanli N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
CC McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
CC Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
CC RT "Complete genome sequence of Methanobacterium thermoautotrophicum
CC deltaH: functional analysis and comparative genomics.";
CC RL J. Bacteriol. 179:7135-7155(1997).
CC CC -!- SIMILARITY: Belongs to the UPF0280 family.
CC
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CC
CC EMBL; AE000852; AAB85232.1; -.
CC PIR; B69197; B69197.
CC HAMAP; MF_01079; 1.
CC DR InterPro; IPR007183; DUF375.
CC DR Pfam; PF04040; DUF375; 1.
CC
```

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; 15 000 5.11 length

Db 114 SSKFFEE 120

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FT 43 L -> P (IN REF. 4).
CONFLICT 99 E -> G (IN REF. 3).
CONFLICT 122 V -> F (IN REF. 2).
SEQUENCE 294 AA; 32459 MW; 9DSF32D67ABCS3EA CRC64;

Query Match 1.7%; Score 7; DB 1; Length 294;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

146 THRLEHS 152
|||||
222 THRLEHS 228

RESULT 22
OSBL BORBU
IID OSBL BORBU STANDARD; PRT: 296 AA.
AC P17739; Q50909; Q44963; Q44965; Q44966; Q44968; Q44970; Q44972;
AC Q44975; Q57510;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer surface protein B precursor.
DE OSPB OR BBA16.
GN Borrelia burgdorferi (Lyme disease spirochete).
OS
OG Plasmid lp54.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OC NCBI_Taxid=139;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=ATCC 35210 / B31;
RC MEDLINE=89343634; PubMed=2761388;
RX Bergstrom S., Bundoc V., Barbour A.G.;
RA "Molecular analysis of linear plasmid-encoded major surface proteins,
RT OspA and OspB, of the Lyme disease spirochaete Borrelia
RT burgdorferi.";
RL Mol. Microbiol. 3:479-486(1989).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=Various strains;
RC MEDLINE=94166630; PubMed=8121286;
RX Caporale D.A., Kocher T.D.;
RA "sequence variation in the outer-surface-protein genes of Borrelia
RT burgdorferi.";
RL Mol. Biol. Evol. 11:51-64(1994).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN=HB19;
RC MEDLINE=9422578; PubMed=7513309;
RX Sadzlene A., Jonsson M., Bergstrom S., Bright R.K., Kennedy R.C.,
RA Barbour A.G.;
RA "A bactericidal antibody to Borrelia burgdorferi is directed against
RT a variable region of the OspB protein.";
RL Infect. Immun. 62:2037-2045(1994).
RN [4]
RP SEQUENCE FROM N.A.
RP STRAIN=ATCC 35210 / B31;
RC MEDLINE=98065943; PubMed=9403685;
RX Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Karpavich A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uitterlinden T., Wathley L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RN "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi";
RL Nature 390:580-586(1997).
RN CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor.
CC
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CC -----

DR EMBL; X14407; CAA32580.1; -
DR EMBL; L23136; AAA22952.1; -
DR EMBL; L23137; AAA22954.1; -
DR EMBL; L23138; AAA20948.1; -
DR EMBL; L23139; AAA20950.1; -
DR EMBL; L23140; AAA20952.1; -
DR EMBL; L23141; AAA20954.1; -
DR EMBL; L23142; AAA20956.1; -
DR EMBL; L23143; AAA20958.1; -
DR EMBL; L23144; AAA20960.1; -
DR EMBL; L31399; AAA63758.1; -
DR EMBL; AE000790; AAC66243.1; -
DR PIR; I40250; I40250.
DR PIR; I40252; I40252.
DR PIR; I40256; I40256.
DR PIR; I40260; I40260.
DR PIR; I40264; I40264.
DR TIGR; BBA16; -
DR InterPro; IPR001809; Outsurface.
DR InterPro; IPR000437; Prok_lipoprot_s.
DR Pfam; PF00820; Lipoprotein_1; 1.
DR PRINTS; PRO0968; OUTSURFACE.
DR ProDom; PD001127; Outsurface; 1.
DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
KW Outer membrane; Lipoprotein; Signal; Plasmid; Complete proteome;
KW Palmitate.
FT SIGNAL 1 15
FT CHAIN 16 296
FT LIPID 16 16
FT LIPID 16 16
FT LIPID 16 16
FT VARIANT 42 42
FT VARIANT 89 89
FT VARIANT 123 123
FT VARIANT 126 126
FT VARIANT 128 128
FT VARIANT 128 128
FT VARIANT 132 132
FT VARIANT 176 176
FT VARIANT 189 189
FT VARIANT 192 192
FT VARIANT 198 198
FT VARIANT 218 218
FT VARIANT 253 253
FT VARIANT 253 253
FT CONFLICT 12 12
FT CONFLICT 214 214
FT CONFLICT 296 AA; 31774 MW; 4A11D0AA6882310E CRC64;
SQ SEQUENCE 296 AA; 31774 MW; 4A11D0AA6882310E CRC64;
Query Match 1.7%; Score 7; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
Db 212 LKREIEK 218
RESULT 23
COAA_STRP3 STANDARD; PRT; 306 AA.
ID COAA_STRP3
AC Q8K7C7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pantothenate Kinase (EC 2.7.1.33) (Pantothenic acid kinase).
GN COAA OR SPYM3_0871 OR SP51071.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RX MEDLINE=22683278; PubMed=12799345;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayaishi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055 (2003).
CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the prokaryotic pantothenate kinase family.
CC -----
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CC -----
DR EMBL; AE014154; AAM79478.1; -
DR EMBL; AP005144; BAC64166.1; -
DR HAMAP; MF 00215; -; 1.
DR InterPro; IPR004566; Pank_bact.
DR InterPro; IPR006083; PRK_URK.
DR Pfam; PF00485; PRK; 1
DR PIRSF; PIRSF000545; Pantothenate_kin; 1.
DR Transferrase; Kinase; ATP-binding; Coenzyme A biosynthesis;
KW Complete proteome.
FT NP BIND 91 98 ATP (POTENTIAL).
SQ SEQUENCE 306 AA; 35608 MW; 923271A925833C7 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 QEELKSI 229
Db 29 QEELKSI 35
RESULT 24
COAA_STRP8 STANDARD; PRT; 306 AA.
ID COAA_STRP8
AC Q8POV9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pantothenate Kinase (EC 2.7.1.33) (Pantothenic acid kinase).

```

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
-!- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-phosphopantothenate.
-!- PATHWAY: Coenzyme A [CoA] biosynthesis; first step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable)".
-!- SIMILARITY: Belongs to the prokaryotic pantothenate kinase family.
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EMBL; AB006563; AAK34090.1; -.
HMAP; MF_00215; -. 1.
InterPro; IPR004566; Pank_bact.
InterPro; IPR006083; PRK_URK.
Pfam; PF00485; PRK; 1.
PIRSF; PIRSF000545; Pantothenate_kin; 1.
Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis; Complete proteome.
NP_BIND 91 ATP (POTENTIAL).
SEQUENCE 306 AA; 35609 MW; 6230FD2725EGSEA4 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 306;
Best Local Similarity 100.0%; Pred.No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 223 QEELKSI 229
| | | | |
DB 29 QEELKSI 35
-----
RESULT 26
Y04O_BPT4 STANDARD; PRT; 308 AA.
ID Y04O BPT4
AC P39254;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypoetical 36.3 kDa protein in nrdC-mobD intergenic region.
Y04O OR NRDC.3.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
NCBI TaxID=10665;
[1]
RN SEQUENCE FROM N.A.
RP Kzhavina N., Marusch E., Djavakhishvili T., Neitzel J., Peterson S.,
RA Awaya M., Edemiller J., Canada D., Tracy J., Gallbreath K.,
RA Paddison P., Anderson B., Stidham T., Blattner F., Kutler E.M.;
RT "The 10.7 kb 'nonessential' region of bacteriophage T4 between the
RT genes tk and nrdC: twenty new t4 genes, generally conserved among
RT T-even phages."
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP MESLINE=22514363; PubMed=12626685;
RX Miller E.S., Kutler E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 Genome.";
R Microbiol. Mol. Biol. Rev. 67:86-156(2003).
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EMBL; U76612; AAB26979.1; -.

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DR EMBL; AF158101; AAD42631.1; -.
KW Hypothetical protein.
SQ SEQUENCE 308 AA; 36293 MW; 4FCF8D4A46061A59 CRC64;

Query Match
Best Local Similarity 1.7%; Score 7; DB 1; Length 308;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 FKRSLL 363
DB 65 FKRSLL 71

RESULT 27
OZB2 HUMAN STANDARD; PRT; 322 AA.
AC Q8NGI1.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 56B2.
GN OR56B2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols";
CC
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CC
CC EMBL; AB063814; BAC06033.1; -.
CC Genew; HGNC:15246; OR56B2.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Olfaction.
CC DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 35 55 1 (POTENTIAL).
CC FT DOMAIN 56 63 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 64 84 2 (POTENTIAL).
CC FT DOMAIN 85 108 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 109 129 3 (POTENTIAL).
CC FT DOMAIN 130 148 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 149 169 4 (POTENTIAL).
CC FT DOMAIN 170 205 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 206 226 5 (POTENTIAL).
CC FT DOMAIN 227 245 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 247 267 6 (POTENTIAL).
CC FT DOMAIN 268 281 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 282 302 7 (POTENTIAL).
CC FT DOMAIN 303 322 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 106 198 BY SIMILARITY.
CC FT CARBOHYD 12 12 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 322 AA; 35955 MW; CFA12F613D1EEF5B CRC64;
SQ
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Query Match
Best Local Similarity 1.7%; Score 7; DB 1; Length 322;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 PSIIIES 143
DB 142 PSIIIES 148

RESULT 28
RBSR_BACHD STANDARD; PRT; 331 AA.
AC Q9K6K2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ribose operon repressor.
GN RBSR OR BH3727.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C-125 / JCM 9153;
RA MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -!- FUNCTION: Transcriptional repressor for the ribose rbsADCBK
CC operon (By similarity).
CC -!- SIMILARITY: Contains 1 HTH lacI-type DNA-binding domain.
CC
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CC
CC EMBL; AP001519; BAB07446.1; -.
CC HSP; P15039; IPRU.
CC InterPro; IPR000843; HTH_LacI
CC Pfam; PF00356; lacI; 1.
CC PRINTS; PR00036; HTHLACI.
CC SMART; SM00354; HTH_LACI; 1.
CC PROSITE; PS00356; HTH_LACI_1; 1.
CC PROSITE; PS00356; HTH_LACI_2; 1.
CC Transcription regulation; Repressor; DNA-binding; Complete proteome.
CC DOMAIN 1 56 HTH_LACI-TYPE.
CC DNA BIND 4 23 H-T-H MOTIF (POTENTIAL).
CC SEQUENCE 331 AA; 36637 MW; DF228BD875BF607F CRC64;

Query Match
Best Local Similarity 1.7%; Score 7; DB 1; Length 331;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
DB 97 TDEIEK 103

RESULT 29
KDGT_ERWCH STANDARD; PRT; 339 AA.
ID KDGT_ERWCH
AC P15701;
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DT 01-APR-1990 (Rel. 14, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 2-keto-3-deoxygluconate permease (KDG permease).
GN KDG.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90060835; PubMed=2684787;
RA Allen C., Reverchon S., Robert-Baudouy J.;
RT "Nucleotide sequence of the Erwinia chrysanthemi gene encoding
RT 2-keto-3-deoxygluconate permease.";
RL Gene 83:233-241(1989).
CC -!- FUNCTION: The 2-keto-3-deoxygluconate permease transports the
CC degraded pectin products into the bacterial cell, where they serve
CC as carbon and energy sources. This is a hydrogen coupled transport
CC system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: Belongs to the kdg transporter family.
CC
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CC
CC EMBL; M31456; AAA83925.1; ALT_INIT.
DR PIR; JQ0113; JQ0113.
DR HAMAP; MF_00070; -.
DR InterPro; IPR004684; KdgT.
DR Pfam; PF03812; KdgT; 1.
DR TIGRfam; TIGR00993; kdgT; 1.
KW Transport; Sugar transport; Symport; Inner membrane; Transmembrane.
FT TRANSMEM 10 30
FT TRANSMEM 42 62
FT TRANSMEM 77 97
FT TRANSMEM 100 120
FT TRANSMEM 141 161
FT TRANSMEM 163 183
FT TRANSMEM 199 219
FT TRANSMEM 224 244
FT TRANSMEM 254 274
FT TRANSMEM 289 309
FT TRANSMEM 339 345
SQ SEQUENCE 339 AA; 35037 MW; 9AD38FFDF67F475 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 FSRVQT 197
Db 195 FSRVQT 201

RESULT 30
RDS2_XENLA
ID_RDS2_XENLA STANDARD; PRT; 345 AA.
AC Q42582;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RDS/peripherin-like protein XRD336.
GN RDS36.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

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RN SEQUENCE FROM N.A.
RX MEDLINE=97081973; PubMed=8923216;
RA Kedzierski W., Moghrabi W.N., Allen A.C., Jablonski-Stienke M.M.,
RA Azarian S.M., Bok D., Travis G.H.;
RT "Three homologs of rds/peripherin in Xenopus laevis photoreceptors
RT that exhibit covalent and non-covalent interactions.";
RL J. Cell Sci. 109:2551-2560(1996).
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Rod specific.
CC -!- SIMILARITY: Belongs to the RDS (peripherin) / ROM1 family.
CC
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CC
CC EMBL; L79914; AAB64232.1; -.
DR InterPro; IPR000830; RDS_ROM.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Transmembrane4; 1.
DR PRINTS; PR00218; PERIPHERNRDS.
DR PROSITE; PS00930; RDS_ROM1; 1.
KW Photoreceptor; Vision; Transmembrane; Glycoprotein.
FT DOMAIN 1 24
FT TRANSMEM 25 43
FT TRANSMEM 44 61
FT DOMAIN 62 80
FT TRANSMEM 81 99
FT TRANSMEM 100 123
FT DOMAIN 124 264
FT TRANSMEM 265 290
FT TRANSMEM 291 345
FT DOMAIN 345 54
FT CARBOHYD 54 54
FT CARBOHYD 229 229
FT SEQUENCE 345 AA; 38726 MW; DF8F0BC2FB8DF778 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 DTGFL 34
Db 302 DTGFL 308

RESULT 31
PGL1_COLLN
ID_PGL1_COLLN STANDARD; PRT; 363 AA.
AC Q00446;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endopolygalacturonase 1 precursor (EC 3.2.1.15) (pectinase) (clpgl).
GN PGL1.
OS Colletotrichum lindemuthianum (Anthracnose fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Incertae sedis; Phyllachorales; Phyllachoraceae;
OC mitosporic Phyllachoraceae; Colletotrichum.
OX NCBI_TaxID=5458;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96200868; PubMed=8621072;
RA Centis S., Dumas B., Fournier J., Marolda M., Esquerre-Tugaye M.T.;
RT "Isolation and sequence analysis of Clpgl, a gene coding for an
RT endopolygalacturonase of the phytopathogenic fungus Colletotrichum
RT lindemuthianum.";
RL Gene 170:125-129(1996).
CC -!- FUNCTION: Involved in maceration and soft-rotting of plant tissue.

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CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
CC
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CC
CC -----
CC EMBL; X89370; CAA6152.1; -.
CC PIR; JC4748; JC4748.
CC InterPro; IPR000743; Glyco_hydro_28.
CC InterPro; IPR006626; Pbh1.
CC Pfam; PF00295; Glyco_hydro_28; 1.
CC SMART; SM00710; Pbh1_4
CC PROSITE; PS00502; POLYGLACTURONASE; 1.
CC Hydrolase; Glycosidase; Cell wall; Signal; Zymogen; Multigene family;
CC Glycoprotein.
CC SIGNAL 1 17 POTENTIAL.
CC FT PROPEP 18 26 POTENTIAL.
CC FT CHAIN 27 363 ENDOPOLYGLACTURONASE 1.
CC FT ACT_SITE 224 224 PROBABLE.
CC FT CARBOXID 212 212 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 363 AA; 36712 MW; A17A60386791B897 CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 363;
CC Best Local Similarity 100.0%; Pred. No. 50;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 13 FVLGALA 19
CC Db 6 FVLGALA 12
CC
CC RESULT 32
CC NUZM_METSE STANDARD; PRT; 385 AA.
CC AC 047495;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
CC ND2.
CC Metridium senile (Brown sea anemone) (Frilled sea anemone).
CC Mitochondrion.
CC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
CC Nymphaeae; Metridiidae; Metridium.
CC NCBI_TaxID=6116;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=White morph;
CC Beagley C.T., Okimoto R., Wolstenholme D.R.;
CC Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.
CC
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CC
CC -----
CC EMBL; AF000023; AAC04638.1; -.
CC PIR; T11892; T11892.
CC InterPro; IPR001750; Oxidored_q1.
CC DR

DR Pfam; PF00361; oxidored_q1; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 385 AA; 40974 MW; A0A4A67F7B373134 CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 385;
CC Best Local Similarity 100.0%; Pred. No. 52;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 13 FVLGALA 19
CC Db 66 FVLGALA 72
CC
CC RESULT 33
CC YG18_AQUAE STANDARD; PRT; 413 AA.
CC ID YG18_AQUAE
CC AC 067545;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Hypothetical protein AQ_1618.
CC GN AQ_1618.
CC OS Aquifex aeolicus.
CC OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
CC OX NCBI_TaxID=63363;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=VF5;
CC MEDLINE=98196666; PubMed=9537320;
CC Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
CC Graham D.E., Overbeek R., Shear M.A., Kellar M., Aulay M., Huber R.,
CC Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
CC "The complete genome of the hyperthermophilic bacterium Aquifex
CC aeolicus";
CC RT Nature 392:353-358 (1998).
CC RL Nature 392:353-358 (1998).
CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC
CC -----
CC EMBL; AE000748; AAC07516.1; -.
CC PIR; G70439; G70439.
CC InterPro; IPR004477; ComEC_N-term.
CC Pfam; PF03772; Competence_1.
CC TIGRFAWS; TIGR00360; ComEC_N-term; 1. Complete proteome.
CC KW Hypothetical protein; Transmembrane; Complete proteome.
CC FT TRANSMEM 10 32 POTENTIAL.
CC FT TRANSMEM 162 184 POTENTIAL.
CC FT TRANSMEM 189 211 POTENTIAL.
CC FT TRANSMEM 232 254 POTENTIAL.
CC FT TRANSMEM 259 276 POTENTIAL.
CC FT TRANSMEM 288 310 POTENTIAL.
CC FT TRANSMEM 325 347 POTENTIAL.
CC SQ SEQUENCE 413 AA; 47050 MW; 526A96D93CE4EE39 CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 413;
CC Best Local Similarity 100.0%; Pred. No. 56;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 87 KILSNVK 93
CC Db 368 KILSNVK 374
CC
CC RESULT 34
CC GAC1_HUMAN STANDARD; PRT; 465 AA.
CC ID GAC1_HUMAN
CC AC Q8N1C3;
CC DR

28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Gamma-aminobutyric-acid receptor gamma-1 subunit precursor (GABA(A) receptor).
GABRG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: GABA, the major inhibitory neurotransmitter in the
vertebrate brain, mediates neuronal inhibition by binding to the
GABA/benzodiazepine receptor and opening an integral chloride
channel.
CC -!- SUBUNIT: Generally pentameric. There are five types of GABA(A)
receptor chains: alpha, beta, gamma, delta, and rho.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: This subunit carries the benzodiazepine binding
site.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC
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CC
CC EMBL; BC031087; AAH31087.1; -
CC MIM; 137166; -
CC InterPro; IPR005438; GABRG1_receptor.
CC InterPro; IPR005437; GABRG1_receptor.
CC InterPro; IPR006029; Neu_chan_memb.
CC InterPro; IPR006202; Neur_chan_IED.
CC InterPro; IPR006201; Neur_Channel.
CC Pfam; PF02931; Neur_chan_IED; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
CC PRINTS; PR01620; GABAARGAMMA.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGRFAMs; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Multigene family; Transmembrane; Chloride channel.
FT SIGNAL 1 35 POTENTIAL
FT CHAIN 36 465 GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1
FT SUBUNIT.

FT DOMAIN 36 272 EXTRACELLULAR (PROBABLE).
FT TRANSMEM 273 294 PROBABLE.
FT TRANSMEM 299 320 PROBABLE.
FT TRANSMEM 332 354 PROBABLE.
FT DOMAIN 355 444 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 445 465 PROBABLE.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 186 202 BY SIMILARITY.
SQ SEQUENCE 465 AA; 53667 MW; 6C314C955704F855 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 465;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130 LVFLLLT 136
DB 23 LVFLLLT 29
RESULT 35
ID DLDH HALVO STANDARD; PRT; 474 AA.
AC Q04829;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Dihydrolipoamide dehydrogenase (EC 1.8.1.4).
GN LPD.
OS Halobacterium volcanii (Haloflex volcanii).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloflex.
OX NCBI_TaxID=2246;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 325-347.
RC STRAIN=ATCC 29605;
RX MEDLINE=93119588; PubMed=1339281;
RA Vettakkorumakav N.N., Stevenson K.J.;
RT "Dihydrolipoamide dehydrogenase from Haloflex volcanii: gene cloning,
RT complete primary structure, and comparison to other dihydrolipoamide
RT dehydrogenases";
RL Biochem. Cell Biol. 70:70-75(1992).
RN [2]
RP SEQUENCE OF 1-48.
RX MEDLINE=92255933; PubMed=1581034;
RA Vettakkorumakav N.N., Danson M.J., Hough D.W.;
RT "Dihydrolipoamide dehydrogenase from the halophilic archaeobacterium
RT Haloflex volcanii: characterization and N-terminal sequence";
RL Biochem. Cell Biol. 70:70-75(1992).
CC -!- CATALYTIC ACTIVITY: Dihydrolipoamide + NAD(+) = lipoamide + NADH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-I pyridine nucleotide-disulfide
oxidoreductase family.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L09733; AAA72340.1; -
CC PIR; A56824; A56824.
CC HSP; P11959; IEBD.
CC InterPro; IPR001327; FAD_pyr_redox.
CC InterPro; IPR000815; Hg_reductase.
CC InterPro; IPR006258; Lipoamide_dh.
CC InterPro; IPR000205; NAD_BS.

DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR004099; Pyr_redox.dim.
DR InterPro; IPR00103; Pyridine_redox_2.
DR Pfam; PF00070; pyr_redox; 1.
DR Pfam; PF02852; pyr_redox.dim; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00945; HGRDTSASEI.
DR PRINTS; PR00411; PNRDRTASEI.
DR PRINTS; PR00469; PNRDRTASEII.
DR ProDom; PD000139; FAD_pyr_redox; 1.
DR TIGRFAMs; TIGR01350; lipamide DH; 1.
DR PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
DR Redox-active center; Glycolysis; Oxidoreductase; NAD; Flavoprotein;
KW FAD.
KW INIT MET 0 0
FT NP_BIND 38 46 FAD (ADP PART) (BY SIMILARITY).
FT DISULFID 46 51 REDOX-ACTIVE (BY SIMILARITY).
FT ACT_SITE 450 450 PROTON ACCEPTOR/DONOR (BY SIMILARITY).
SQ SEQUENCE 474 AA; 49856 MW; DD790180B913605A CRC64;

Query Match 1.7%; Score 7; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SGFVLGA 17
Db 410 SGFVLGA 416

RESULT 36
ID IF3Y YEAST STANDARD; PRT; 478 AA.
AC P41814;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Eukaryotic translation initiation factor 3 62 kDa subunit (eIF3 p62)
DE (Translation initiation factor eIF3, p62 subunit) (GCD10 protein).
DE GCD10 OR TIF33 OR YNL062C OR N2422.
GN Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Bergz P., Doignon F., Crouzet M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBSJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=S288c / FY1676;
RA Bergz P., Doignon F., Crouzet M.;
RL The sequence of a 44 420 bp fragment located on the left arm of
RT chromosome XIV from Saccharomyces cerevisiae.;
RL Yeast 11:967-974 (1995).
[3]
RN ERRATUM.
RP MEDLINE=97060022; PubMed=8904343;
RA Bergz P., Doignon F., Crouzet M.;
RL Yeast 12:297-297 (1996).
CC -!- FUNCTION: EIF-3 DISOCIATES RIBOSOMES, PROMOTES INITIATOR MET-TRNA
CC AND MRNA BINDING. NEGATIVE REGULATOR OF GCN4 TRANSLATION.
CC -!- SUBUNIT: eIF-3 is composed of up to 8 different subunits.
CC -!- SIMILARITY: BELONGS TO THE EIF-3 P62 FAMILY.
CC
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CC
DR EMBL; X83511; CAA58501.1; -
DR EMBL; U2141; AAA9649.1; -
DR EMBL; Z71338; CAA95935.1; -
DR PIR; S51669; S51669.
DR GerMOnline; 143068; -
DR SGD; S0005006; GCD10.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0008175; P:RNA methyltransferase activity; IDA.
DR GO; GO:0030488; P:RNA methylation; IDA.
DR InterPro; IPR007316; EIF3_gamma.
DR Pfam; PF04189; eif3_gamma; 1.
KW Initiation factor; Protein biosynthesis.
KW SEQUENCE 478 AA; 54389 MW; 99790A1AAC8E8609 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIEKMK 398
Db 142 EEIEKMK 148

RESULT 37
ID MURC VIBCH STANDARD; PRT; 486 AA.
AC Q9KPG8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
DE acetylmuramoyl-L-alanine synthetase).
DE MURC OR VC2400.
GN Vibrio cholerae.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Emolaeva M.D., Vamathevan J., Bass S., Olin H., Dragoi I., Sellers P.,
RA McDonald L., Uterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RL "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483 (2000).
CC -!- FUNCTION: Cell wall formation.
CC -!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine +
CC phosphate + UDP-N-acetylmuramoyl-L-alanine.
CC -!- PATHWAY: Peptidoglycan biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the murCDEF family.
CC
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CC EMBL; AE004310; AAF95543.1; ALT_INIT.
DR TIGR; VC2400; -
DR HAVAP; MF 00046; -; 1.
DR InterPro; IPR000713; Mur_ligase.
DR InterPro; IPR004101; Mur_ligase_C.
DR InterPro; IPR005758; MurC.

DR Pfam: PF01225; Mur ligase; 1.
DR Pfam: PF02875; Mur_ligase C; 1.
DR TIGRfams: TIGR01082; murC; 1.
KW Ligase; ATP-binding; Cell division; Cell wall;
KW Peptidoglycan synthesis; Complete proteome.
FT NP_BIND 129 135 ATP (POTENTIAL).
SQ SEQUENCE 486 AA; 53041 MW; A7AD92DF74ADB4 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 IQAREK 268
DB 98 IQAREK 104

RESULT 38
GCSB_STAAM STANDARD; PRT; 490 AA.
ID GCSB_STAAM
AC Q99TV9;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable glycine dehydrogenase [decarboxylating] subunit 2
DE (EC 1.4.4.2) (Glycine decarboxylase subunit 2) (Glycine cleavage
DE system P-protein subunit 2).
GN GCVPB OR SAV1535 OR SA1365.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878; 158879;
RN
SEQUENCE FROM N.A.
RP STRAIN=Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kishida S., Goto S., Kubozaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus".
RL Lancet 357:1225-1240(2001).
CC
CC -!- FUNCTION: The glycine cleavage system catalyzes the degradation of
CC glycine. The P protein binds the alpha-amino group of glycine
CC through its pyridoxal phosphate cofactor; CO(2) is released and
CC the remaining methylene moiety is then transferred to the
CC lipamide cofactor of the H protein (By similarity).
CC
CC -!- CATALYTIC ACTIVITY: Glycine + lipoylprotein = S-
CC anionomethylidihydropyridoylprotein + CO(2).
CC
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC
CC -!- SUBUNIT: The glycine cleavage system is composed of four proteins:
CC P, T, L and H. In this organism, the P 'protein' is an heterodimer
CC of two subunits (By similarity).
CC
CC -!- SIMILARITY: Belongs to the gcvp family. C-terminal subunit
CC subfamily.
CC
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CC
CC -----
CC EMBL; AP003362; BAB57697.1; -;
CC DR EMBL; AP003362; BAB57697.1; -;
CC DR EMBL; AP003362; BAB57697.1; -;
CC DR PIR; F89933; F89933.
CC DR SWISS-2DPAGE; Q99TV9; STAA.
CC DR HAMAP; MF_00713; -; 1.

DR InterPro: IPR003437; GDC-P.
DR Pfam: PF02347; GDC-P; 1.
KW Oxidoreductase; Pyridoxal phosphate; Complete proteome.
FT BINDING 273 273 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 490 AA; 54783 MW; 6EC8CCBA16D35CBF CRC64;

Query Match 1.7%; Score 7; DB 1; Length 490;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLQEELK 227
DB 119 SLQEELK 125

RESULT 39
GCSB_STAAM STANDARD; PRT; 490 AA.
ID GCSB_STAAM
AC QANW0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable glycine dehydrogenase [decarboxylating] subunit 2
DE (EC 1.4.4.2) (Glycine decarboxylase subunit 2) (Glycine cleavage
DE system P-protein subunit 2).
GN GCVPB OR MW1487.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN
SEQUENCE FROM N.A.
RP MEDLINE=22040717; PubMed=12044378;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yanamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA".
RL Lancet 359:1819-1827(2002).
CC
CC -!- FUNCTION: The glycine cleavage system catalyzes the degradation of
CC glycine. The P protein binds the alpha-amino group of glycine
CC through its pyridoxal phosphate cofactor; CO(2) is released and
CC the remaining methylene moiety is then transferred to the
CC lipamide cofactor of the H protein (By similarity).
CC
CC -!- CATALYTIC ACTIVITY: Glycine + lipoylprotein = S-
CC anionomethylidihydropyridoylprotein + CO(2).
CC
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC
CC -!- SUBUNIT: The glycine cleavage system is composed of four proteins:
CC P, T, L and H. In this organism, the P 'protein' is an heterodimer
CC of two subunits (By similarity).
CC
CC -!- SIMILARITY: Belongs to the gcvp family. C-terminal subunit
CC subfamily.
CC
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CC
CC -----
CC EMBL; AP004827; BAB95352.1; -;
CC DR HAMAP; MF_00713; -; 1.
CC DR InterPro: IPR003437; GDC-P.
CC DR Pfam; PF02347; GDC-P; 1.
KW Oxidoreductase; Pyridoxal phosphate; Complete proteome.
FT BINDING 273 273 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 490 AA; 54782 MW; 6EC8CCBA16D35CB1 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 490;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLQEELK 227

```
Db 119 SLOELK 125
|||||
ID TY3H PHASP STANDARD; PRT; 491 AA.
AC P11982.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
GN TH.
OS Phasianidae sp. (Quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae.
OX NCBI_TaxID=9006;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RX MEDLINE=88089590; PubMed=2447231;
RA Fauguet M., Grima B., Lamouroux A., Mallet J.;
RT "Cloning of quail tyrosine hydroxylase; amino acid homology with
other hydroxylases discloses functional domains.";
RL J. Neurochem. 50:142-148(1988).
CC -!- FUNCTION: Plays an important role in the physiology of adrenergic
neurons.
CC -!- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-
dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
CC -!- COFACTOR: Ferrous ion.
CC -!- ENZYME REGULATION: Phosphorylation leads to an increase in the
catalytic activity.
CC -!- PATHWAY: Catecholamine biosynthesis; first step.
CC -!- SIMILARITY: Belongs to the bipterin-dependent aromatic amino acid
hydroxylase family.
CC
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CC
EMBL; M24778; AAA49514.1; -.
DR F1R; A28582; A28582.
DR HSP; P04177; ITOH.
DR InterPro; IPR001273; Aaa hydroxylase.
DR Pfam; PF00351; bioterin_H_1.
DR PRINTS; PR00372; FYWYDRXLASE.
DR ProDom; PD002559; Aaa hydroxylase; 1.
DR TIGRFAMs; TIGR01269; Tyr_3_monoox; 1.
DR PROSITE; PS00367; BIOTERIN_HYDROXYL; 1.
KW Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
KW Neurotransmitter biosynthesis; Phosphorylation.
FT MOD_RES 40 40 POLY-ALA.
FT DOMAIN 51 55 POLY-ALA.
FT METAL 324 324 IRON (BY SIMILARITY).
FT METAL 329 329 IRON (BY SIMILARITY).
FT METAL 369 369 IRON (BY SIMILARITY).
SQ SEQUENCE 491 AA; 56066 MW; AFB363220F70C0A0 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 390 TDEIEK 396
Db 353 TDEIEK 359
|||||
RESULT 41
Query Match 1.7%; Score 7; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 390 TDEIEK 396
Db 353 TDEIEK 359
|||||
YSMS CAEL STANDARD; PRT; 498 AA.
ID Q10125;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE Hypothetical protein F52C9.5 in chromosome III.
GN F52C9.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pavello A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC
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CC
EMBL; U39850; AAA81055.1; -.
DR F1R; T16417; T16417.
DR WormPep; F52C9.5; CE01963.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR Pfam; PF00024; PAN; 2.
DR SMART; SM00473; PAN_AP; 2.
KW Hypothetical protein.
SQ SEQUENCE 498 AA; 56303 MW; D748EC5752DB35B1 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 357 FKSRLL 363
Db 491 FKSRLL 497
|||||
RESULT 42
ID GCSB STAE STANDARD; PRT; 502 AA.
AC Q8CMM1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Probable glycine dehydrogenase [decarboxylating] subunit 2
(DE EC 1.4.4.2) (Glycine decarboxylase subunit 2) (Glycine cleavage
system P-protein subunit 2).
GN GCVPB OR SE1220.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
CC -!- FUNCTION: The glycine cleavage system catalyzes the degradation of
glycine. The P protein binds the alpha-amino group of glycine
through its pyridoxal phosphate cofactor; CO(2) is released and
the remaining methanamine moiety is then transferred to the
```

CC lipoamide cofactor of the H protein (By similarity).
CC -!- CATALYTIC ACTIVITY: Glycine + lipoylprotein = S-
CC aminomethylidihydrolipoylprotein + CO(2).
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- SUBUNIT: The glycine cleavage system is composed of four proteins:
CC P, T, L and H. In this organism, the P 'protein' is an heterodimer
CC of two subunits (By similarity).
CC -!- SIMILARITY: Belongs to the gcvp family. C-terminal subunit
CC subfamily.
CC
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CC
CC EMBL; AB016748; AA004819.1; -
CC HAMAP; MF_00713; -; 1.
CC InterPro; IPR003437; GDC-P.
CC Pfam; PF02347; GDC-P; 1.
KW Oxidoreductase; Pyridoxal phosphate; Complete proteome.
FT BINDING 273 273 Pyridoxal phosphate (BY SIMILARITY).
SQ SEQUENCE 502 AA; 56402 MW; 48662D78926187A1 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 502;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 221 SLOPELK 227
DB 119 SLOPELK 125
|||||
RESULT 43
VRK2 HUMAN
ID VRK2 HUMAN STANDARD; PRT; 508 AA.
AC Q86Y07; Q86Y08; Q86Y09; Q86Y10; Q86Y11; Q86Y12; Q81X15; Q99987;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase VRK2 (EC 2.7.1.37) (Vaccinia-related
DE kinase 2).
GN VRK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=98008921; PubMed=9344656;
RA Nezu J.-I., Oku A., Jones M.H., Shimane M.;
RT "Identification of two novel human putative serine/threonine kinases,
RT VRK1 and VRK2, with structural similarity to Vaccinia virus B1R
RT kinase.";
RL Genomics 45:327-331(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Blanco S., Klimakova L., Santos C., Sevilla A., Lazo P.A.;
RT "Expression of a variant isoform of the human vaccinia-related kinase
RT 2 (VRK2B) and its effects on p53 dependent transcription.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4 AND 5), AND VARIANT ILE-167.
RA Suriyappan S.P., Sarfarazi M.;
RT "Identification of 6 different isoforms for Vaccinia-related kinase 2
RT (VRK2) gene.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Pancreas;

RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rowstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Probable serine/threonine kinase (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=1;
CC IsoId=Q86Y07-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q86Y07-2; Sequence=VSP_008537, VSP_008538;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q86Y07-3; Sequence=VSP_008533;
CC Note=No experimental confirmation available;
CC Name=4; Synonyms=5;
CC IsoId=Q86Y07-4; Sequence=VSP_008534;
CC Note=No experimental confirmation available;
CC Name=5; Synonyms=6;
CC IsoId=Q86Y07-5; Sequence=VSP_008535, VSP_008536;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Widely expressed. Highly expressed in fetal
CC liver, skeletal muscle, pancreas, heart, peripheral blood
CC leukocytes and testis.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. VRK
CC subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB000450; BAA19109.1; -
CC EMBL; AJ512204; CAD54446.2; -
CC EMBL; AY228367; AAO73047.1; -
CC EMBL; AY228368; AAO73048.1; -
CC EMBL; AY228369; AAO73049.1; -
CC EMBL; AY228370; AAO73050.1; -
CC EMBL; AY228371; AAO73051.1; -
CC EMBL; AY228372; AAO73052.1; -
CC EMBL; BC027854; AAH27854.1; -
CC HSP; Q06486; ICKT.
CC Genew; HGNC:12719; VRK2.
CC MIM; 602169; -
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser_thr_pkin AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot kinase; 1.
CC SMART; SM00220; S_TKc_1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 FT Transmembrane; Alternative splicing; Polymorphism;
 FT TRANSMEM 487 507 ANCHOR FOR TYPE IV MEMBRANE PROTEIN
 (POTENTIAL).
 FT DOMAIN 29 319 PROTEIN KINASE.
 FT NP_BIND 35 61 ATP (BY SIMILARITY).
 FT ACT_SITE 166 166 BY SIMILARITY.
 FT VARSPLIC 1 23 Missing (in isoform 3).
 FT VARSPLIC 1 118 /FTid=VSP_008533.
 FT VARSPLIC 395 396 Missing (in isoform 4).
 FT VARSPLIC 397 396 /FTid=VSP_008534.
 FT VARSPLIC 397 396 ES -> FR (in isoform 5).
 FT VARSPLIC 397 396 /FTid=VSP_008535.
 FT VARSPLIC 395 400 ESTERR -> GRSLG (in isoform 2).
 FT VARSPLIC 401 508 Missing (in isoform 2).
 FT VARIANT 167 167 /FTid=VSP_008538.
 FT CONFLICT 419 419 V -> I (in QDSNP:1051061).
 FT CONFLICT 419 419 K -> E (IN REF. 3;
 FT SEQUENCE 508 AA; 58126 MW; 157BF8F848511AF4 CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 508;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 83 QALKKIL 89
 DB 307 QALKKIL 313
 RESULT 44
 PNK1_MOUSE
 ID PNK1_MOUSE STANDARD; PRT; 548 AA.
 AC Q8K4K6; Q8D3K1; Q9QXM8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Pantothenate kinase 1 (EC 2.7.1.33) (pantothenic acid kinase 1)
 DE (mPank1) (mPank).
 GN PANK1 OR PANK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
 RX MEDLINE=20092916; PubMed=10625688;
 RA Rock C.O., Calder R.B., Karim M.A., Jackowski S.;
 RT "Pantothenate kinase regulation of the intracellular concentration of
 coenzyme A."; J. Biol. Chem. 275:1377-1383 (2000).
 RL [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1), CHARACTERIZATION, AND ALTERNATIVE
 RP SPLICING.
 RX MEDLINE=22090536; PubMed=12095677;
 RA Rock C.O., Karim M.A., Zhang Y.M., Jackowski S.;
 RT "The murine pantothenate kinase (Pank1) gene encodes two
 differentially regulated pantothenate kinase isozymes."; J.
 RL Gene 291:35-43 (2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gless C., King B., Kochiwa H.,
 Kuhl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Nodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection";
 Nature 409:685-690 (2001).
 RL [4]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP TISSUE=Liver, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Plays a role in the physiological regulation of the
 intracellular CoA concentration.
 CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D'-5'-
 phosphopantothenate.
 CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
 thioesters. Strongly inhibited by acetyl-CoA and by many CoA and
 also inhibited by high concentration of non-esterified CoA
 (CoASH). Isoform 1 is inhibited by high concentration of non-
 esterified CoA (CoASH) and strongly inhibited by acetyl-CoA and by
 malonyl-CoA. Isoform 2 is stimulated by CoA and weakly inhibited
 by acetyl-CoA and malonyl-CoA.
 CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Pank1-alpha;
 CC IsoId=Q8K4K6-1; Sequence=Displayed;
 CC Name=2; Synonyms=Pank1-beta;
 CC IsoId=Q8K4K6-2; Sequence=VSP_004522, VSP_004523;
 CC -1- TISSUE SPECIFICITY: Expressed in liver and kidney. Isoform 1 is
 highly expressed in heart and skeletal muscle, whereas isoform 2
 is expressed exclusively in testis.
 CC -1- DOMAIN: The N-terminal extension, present in isoform 1 may be the
 regulatory domain.
 CC -1- SIMILARITY: Belongs to the eukaryotic pantothenate kinase family.
 CC -----
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DR EMBL; AF200357; AAF23952.1; -;
DR EMBL; AF347700; AAM77216.1; -;
DR EMBL; AK017345; BAB30700.1; -;
DR EMBL; BC023496; AAB23496.1; -;
DR MGD; MGI:1922385; Pank1.
DR GO; GO:0004594; Pantothenate kinase activity; IDA.
DR InterPro; IPR004567; Pank_eukar.
DR Pfam; PF03630; Fumble; 1.
KW Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
KW Alternative splicing.
FT VARSPLIC 1 175 Missing (in isoform 2).
FT FTid=VSP_004522.
FT MDSGEKRP -> MKLVNGRKQT (in isoform 2).
FT FTid=VSP_004523.
SQ SEQUENCE 548 AA; 60091 MW; C916709D048E429B CRC64;

Query Match 1.7%; Score 7; DB 1; Length 548;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 VDKLVKD 246
Db 421 VDKLVKD 427

RESULT 45
ID_PNK1_HUMAN STANDARD; PRT; 598 AA.
AC Q8TE04; Q8TE08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic acid kinase 1)
DE (hPank1) (hPANK).
GN PANK1 OR PANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Fetal brain;
RX MEDLINE=21668246; PubMed=11809413;
RA Ni X., Ma Y., Cheng H., Jiang M., Ying K., Xie Y., Mao Y.;
RT "Cloning and characterization of a novel human pantothenate kinase
gene.";
RL Int. J. Biochem. Cell Biol. 34:109-115(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 460-598 FROM N.A. (ISOFORM 2).
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schestz T.E.,
RA Bawa S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzyzinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
IDENTIFICATION OF ISOFORM 1.
RA Zhou B., Westaway S.K., Levinson B., Johnson M.A., Gitschier J.,
RA Haylick S.J.;
RL Unpublished observations (JUL-2001).
CC -!- FUNCTION: Plays a role in the physiological regulation of the
CC intracellular CoA concentration (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -!- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
CC thioesters. Strongly inhibited by acetyl-CoA and by many CoA and
CC also inhibited by high concentration of non-esterified CoA (COASH)
CC (By similarity).
CC -!- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Pank1-alpha;
CC IsoId=Q8TE04-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8TE04-2; Sequence=VSP_004520;
CC Name=3;
CC IsoId=Q8TE04-3; Sequence=VSP_004520, VSP_004521;
CC -!- TISSUE SPECIFICITY: Expressed in liver and kidney.
CC -!- DOMAIN: The N-terminal extension, present in isoform 1 may be the
CC regulatory domain.
CC -!- SIMILARITY: Belongs to the eukaryotic pantothenate kinase family.
CC -!- CAUTION: Isoform 2, although confirmed in the murine ortholog, is
CC only partially cloned and needs a further complete identification.

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CC EMBL; AF35198; AAL86371.1; -;
CC EMBL; AL157400; -; NOT ANNOTATED CDS.
CC EMBL; BC026296; AAB26296.1; ALT_INIT.
CC EMBL; BK000008; DAA00002.1; -;
CC Genew; HGNC:8598; PANK1.
CC MIM; 606160; -;
CC InterPro; IPR004567; Pank_eukar.
CC Pfam; PF03630; Fumble; 1.
CC Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
KW Alternative splicing.
FT VARSPLIC 1 235
FT FTid=VSP_004520.
FT Missing (in isoform 3).
FT FTid=VSP_004521.
FT N -> D (IN REF. 1).
FT CONFLICT 306 306
SQ SEQUENCE 598 AA; 64339 MW; 0A92115D5BEDFC4C CRC64;

Query Match 1.7%; Score 7; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 VDKLVKD 246
Db 471 VDKLVKD 477

RESULT 46

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DNAX LACSN
ID DNAX LACSN STANDARD; PRT; 614 AA.
AC O8KML6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chapterone protein dnax (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70).
DE DNAX.
GN DNAX.
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 20451;
RA Ehrmann M.A.;
RT Identification and characterization of the dnax operon of Lactobacillus sanfranciscensis.;
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC -----
CC EMBL; AJ315382; CAC86402.1; -.
CC HAMAP; MF_00332; -.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; HSP70; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 176 176 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 614 AA; 66299 MW; DDDDF2AA8875E711 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 391 DEIEKM 397
Db 482 DEIEKM 488
RESULT 47
ASNB BACSU
ID ASNB BACSU STANDARD; PRT; 632 AA.
AC P54420; O34902;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4).
DE ASNB OR ASN OR BSU30540.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
```

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RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruchi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerthof A., Ehrlich S.D., Emerson P.T.,
RA Denicot P., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Ertz C., Ertz J., Fabret C., Ferrarini E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haeche J.J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogasawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeder R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Sarroz P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Tognoni A.,
RA Toseato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "the complete genome sequence of the Gram-positive bacterium Bacillus subtilis";
RL Nature 390:249-256 (1997).
RN [3]
RP SEQUENCE OF 1-81 FROM N.A.
RC STRAIN=168 / PY79;
RX MEDLINE=96345628; PubMed=8755891;
RA Yocum R., Perkins J.B., Howitt C.L., Pero J.;
RT "Cloning and characterization of the metB gene encoding S-adenosylmethionine synthetase from Bacillus subtilis.";
RL J. Bacteriol. 178:4604-4610 (1996).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99429856; PubMed=10498721;
RA Yoshida K.-I., Fujita Y., Ehrlich S.D.;
RT "Three asparagine synthetase genes of Bacillus subtilis.";
RL J. Bacteriol. 181:6081-6091 (1999).
CC -!- FUNCTION: MAIN ASPARAGINE SYNTHETASE IN VEGETATIVE CELLS.
CC -!- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP + diphosphate + L-asparagine + L-glutamate.
CC -!- PATHWAY: Asparagine biosynthesis.
CC -!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC -!- SIMILARITY: Belongs to the asparagine synthetase family.
CC
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CC
CC -----
CC EMBL; AF008220; AAC00243.1; -.
CC F00119; CAB15032.1; -.
CC EMBL; U52812; AAB17067.1; -.
CC PIR; H69590; H69590.
CC HSP; P22106; ICT9.
CC Subtilisin; BGL1831; asnB.
CC InterPro; IPR006426; Asn_synth_AEB.
CC InterPro; IPR001962; Asn_synthase.
CC InterPro; IPR000583; GATase_2.
CC Pfam; PF00733; Asn_synthase; 1.
CC Pfam; PF00310; GATase_2; 1.
CC TIGRfams; TIGR01536; asn_synth_AEB; 1.
```


KW Ligase; Asparagine biosynthesis; Glutamine amidotransferase;
KW Complete proteome.
FT ACT SITE 2 GATASE (BY SIMILARITY).
FT CONFLICT 79 E1Y -> VNL (IN REF. 2).
SQ SEQUENCE 632 AA; 72666 MW; 155F11E6988901EA CRC64;
Query Match 1.7%; Score 7; DB 1; Length 632;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 NTDSDE 30
| | | | |
Db 98 NTDSDE 104
RESULT 48
ID DNAK_BACTN STANDARD; PRT; 638 AA.
AC Q89Y6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chapterone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70).
DE DNAK OR B74615.
GN DNAK
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=819;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RA "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
CC -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC EMBL; AE016945; AA079720.1; --
CC HAMAP; MF_00332; ; 1.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; HSP70; 1.
CC PROSITE; PS00297; HSP70.1; 1.
CC PROSITE; PS00329; HSP70.2; 1.
CC PROSITE; PS01036; HSP70.3; 1.
KW Chapterone; ATP-binding; Heat shock; Phosphorylation;
KW Complete proteome.
FT MOD_RES 197 197 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 638 AA; 68367 MW; 63D7AF53160206D0 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 EIEKMK 398
| | | | |
Db 504 EIEKMK 510
RESULT 49

SENS_HUMAN
ID SENS_HUMAN STANDARD; PRT; 755 AA.
AC Q96H10; Q96SAS;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sentrin-specific protease 5 (EC 3.4.22.-) (Sentrin/SUMO-specific
DE protease SENP5) (Protease FKSG45).
GN SENP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta, and Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RP SEQUENCE OF 305-755 FROM N.A.
RA Wang Y.-Q., Li T.;
RT "Identification of FKSG45, a novel gene located on human chromosome
RT 3.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP REVIEW.
RX MEDLINE=20267842; PubMed=10806345;
RA Yeh E.T.H., Gong L., Kamitani T.;
RT "Ubiquitin-like proteins: new wines in new bottles.";
RL Gene 248:1-14(2000).
CC -!- FUNCTION: Involved in the release of sentrins (Potential).
CC -!- SIMILARITY: Belongs to peptidase family C48.
CC
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CC
CC EMBL; BC008589; AA08589.1; --
CC EMBL; BC030705; AA030705.1; --
CC EMBL; AF335474; AA069630.1; ALT_INT.
CC MEROPS; C48.008; --
CC InterPro; IPR003653; Peptidase_C48.
CC Pfam; PF02902; Peptidase_C48; 1.
CC PROSITE; PS00600; ULP_PROTEASE; 1.
KW Hydrolase; Protease; Thiol protease; Ub1 conjugation pathway.
FT DOMAIN 567 724 PROTEASE
FT ACT_SITE 646 646 BY SIMILARITY.
FT ACT_SITE 663 663 BY SIMILARITY.
FT ACT_SITE 713 713 BY SIMILARITY.
FT CONFLICT 538 538 S -> C (IN REF. 2).
FT

```
SQ SEQUENCE 755 AA; 86733 MW; 1B89228FB56B329 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 755;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 EEDGSLK 210
DB 443 EEDGSLK 449

RESULT 50
SEN5 MACFA
ID SEN5 MACFA STANDARD; PRT; 755 AA.
AC Q8WP32;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sentrin-specific protease 5 (EC 3.4.22.-) (Sentrin/SUMO-specific
protease SENP5) (Q8EA-16408).
GN SENP5
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA Teraso K., Sugano S.;
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
libraries."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the release of sentrins (Potential).
CC -!- SIMILARITY: Belongs to peptidase family C48.
CC
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CC
CC -----
CC EMBL; AB074445; BAB72076.1; -.
CC InterPro; IPR003653; Peptidase_C48.
CC Pfam; PF02902; Peptidase_C48; 1.
CC PROSITE; PS00600; ULP_PROTEASE; 1.
CC Hydrolase; Protease; Thiol protease; Ub1 conjugation pathway.
FT DOMAIN 563 724 PROTEASE
FT ACT_SITE 646 646 BY SIMILARITY.
FT ACT_SITE 663 663 BY SIMILARITY.
FT ACT_SITE 713 713 BY SIMILARITY.
SQ SEQUENCE 755 AA; 86290 MW; 40EC773CA29B8CEA CRC64;

Query Match 1.7%; Score 7; DB 1; Length 755;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 EEDGSLK 210
DB 443 EEDGSLK 449

RESULT 51
NH48_CABEL
ID NH48_CABEL STANDARD; PRT; 780 AA.
AC Q94407; Q9BJL2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nuclear hormone receptor family member nhr-48.
```

```
GN NHR-48 OR ZK662.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA White S.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 262-780 FROM N.A.
RA Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;
RT "Caenorhabditis elegans nuclear receptor sequences exhibit biophysical
compatibility with the ligand-binding domain fold."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Orphan nuclear receptor.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
CC
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CC
CC -----
CC EMBL; Z79604; CAB01900.1; -.
CC EMBL; AF332204; AAK1975.1; -.
CC PIR; T27941; T27941.
CC HSP; P20393; 1A6Y.
CC WormPep; ZK662.3; CE18456.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNA_BIND 100 165 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 100 120 C4-TYPE.
FT ZN_FING 136 160 C4-TYPE.
SQ SEQUENCE 780 AA; 87373 MW; 74922FB93F7D8B40 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 DERIEKM 397
DB 593 DERIEKM 599

RESULT 52
H104_YEAST
ID H104_YEAST STANDARD; PRT; 908 AA.
AC P31539;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Heat shock protein 104.
GN HSP104 OR YLL026W OR L0948.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X2180 / ATCC 26109;
RX MEDLINE=91375541; PubMed=1896074;
```

RA Parsell D.A., Sanchez Y., Stitzel J.D., Lindquist S.;
RT "Hsp104 is a highly conserved protein with two essential nucleotide-
RL binding sites";
RN Nature 353:270-273 (1991).
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Biles L., Albermann K., Andre B., Ansoorge W.,
RA Benes V., Bruckner M., Dalius H., Dubois E., Duesterhoeft A.,
RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
RA Louis E.J., Messenguy F., Meves H.-W., Miosga T., Moestl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Purnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,
RA Schaefer M., Scherrens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendels F., Voet M., Volckaert G., Voss H., Wambutt R., Medler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Honeisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII";
RL Nature 387:87-90 (1997).
RN SEQUENCE OF 749-908 FROM N.A.
RP STRAIN=S288c;
RC MEDLINE=97197984; PubMed=9046100;
RA Purnelle B., Goffeau A.;
RT "The sequence of 32kb on the left arm of yeast chromosome XII reveals
RT six known genes, a new member of the seripauperins family and a new
RT ABC transporter homologous to the human multidrug resistance
RT protein";
RL Yeast 13:183-188 (1997).
CC -!- FUNCTION: Vital for tolerance to heat, ethanol and other stressors.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- SIMILARITY: Belongs to the clpA/clpB family.
CC
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CC
DR EMBL; M67479; AAA50477.1; -;
DR EMBL; Z73131; CAA97475.1; -;
DR EMBL; Z73130; CAA97474.1; -;
DR EMBL; X97560; CAA66164.1; -;
DR PIR; S61476; S61476.
DR GenOnline; 142021; -;
DR SWISS-2DPAGE; P31539; YEAST.
DR SGO; S0003949; HSP104.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0003763; F:chaperonin ATPase activity; IDA.
DR GO; GO:0003767; F:co-chaperone protein activity; IDA.
DR GO; GO:0003773; F:heat shock protein activity; IDA.
DR GO; GO:0006457; P:protein folding; IDA.
DR GO; GO:0006950; P:response to stress; IDA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_Centr.
DR InterPro; IPR001270; Chaprinin_clpA/B.
DR InterPro; IPR004176; Clp_N.
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF02861; Clp_N; 2.
DR PRINTS; PR00300; CLPPROTEASEA.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00870; CLPAB_1; 1.
DR PROSITE; PS00871; CLPAB_2; 1.
DR Chaperone; Heat shock; ATP-binding; Repeat.
FT DOMAIN 167 411
FT NP_BIND 541 731
FT NP_BIND 212 219 ATP (POTENTIAL).
FT NP_BIND 614 621 ATP (POTENTIAL).
FT

SQ SEQUENCE 908 AA; 102034 MW; 4AD0E7E3AF98E318 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 908;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 220 ASLQEEEL 226
DB 453 ASLQEEEL 459
RESULT 53
M3KA HUMAN
ID M3KA HUMAN STANDARD; PRT; 954 AA.
AC Q02779; Q12761; Q14871;
DT 01-FEB-1994 (Rel. 28, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitogen-activated protein kinase kinase 10 (EC 2.7.1.37)
DE (Mixed lineage kinase 2) (Protein kinase MST).
GN MAP3K10 OR MLK2 OR MST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96128179; PubMed=8536694;
RA Dorow D.S., Devereux L., Tu G.F., Price G., Nicholl J.K.,
RA Sutherland G.R., Simpson R.J.;
RT "Complete nucleotide sequence, expression, and chromosomal
RT localisation of human mixed-lineage kinase 2";
RL Eur. J. Biochem. 234:492-500 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95249256; PubMed=7731697;
RA Katoh M., Hirai M., Sugimura T., Terada M.;
RT "Cloning and characterization of MST, a novel (putative)
RT serine/threonine kinase with SH3 domain";
RL Oncogene 10:1447-1451 (1995).
RN [3]
RP SEQUENCE OF 244-480 FROM N.A.
RC TISSUE=Colon epithelium;
RX MEDLINE=93238756; PubMed=8477742;
RA Dorow D.S., Devereux L., Dietzsch E., de Kretser T.;
RT "Identification of a new family of human epithelial protein kinases
RT containing two leucine/isoleucine-zipper domains";
RL Eur. J. Biochem. 213:701-710 (1993).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- TISSUE SPECIFICITY: Expressed in brain and skeletal muscle.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MAP
CC kinase kinase subfamily.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC
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CC
DR EMBL; X90846; CAA62351.1; -;
DR EMBL; Z48615; CAA98531.1; -;
DR PIR; S68178; S68178.
DR HSP; P11362; IFGK.
DR Genew; HGNC:6849; MAP3K10.
DR MIM; 600137; -;
DR GO; GO:0004672; F:protein kinase activity; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0007254; P:JNK cascade; TAS.

RL Mol. Gen. Genet. 256:45-53 (1997).
CC -!- FUNCTION: May function by modifying and partially stabilizing
CC thermolabile DNA polymerases, perhaps during DNA repair.
CC -!- PTM: Autophosphorylated.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC
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CC
CC EMBL: U18516; AAC03227.1; -
CC EMBL: U13398; AAC49840.1; ALT_TERM.
CC PIR: S50632; S50632.
CC GerMOnline: I39208; -
CC SGP: S000931; FAKI.
CC GO: GO:0004672; P:protein kinase activity; IDA.
CC GO: GO:0006261; P:DNA dependent DNA replication; IGI.
CC GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
CC InterPro: IPR000719; Prot_kinase
CC InterPro: IPR008271; Ser_Thr_Pkin_AS.
CC InterPro: IPR003290; Ser_Thr_Pkinase.
CC Pfam: PF00069; Pkinase; 1.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
CC TransPhosBase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 133 448 PROTEIN KINASE.
FT NP_BIND 139 147 ATP (BY SIMILARITY).
FT BINDING 162 162 ATP (BY SIMILARITY).
FT ACT_SITE 277 277 BY SIMILARITY.
FT CONFLICT 171 171 Q -> H (IN REF. 2).
FT CONFLICT 266 268 EYL -> DS (IN REF. 2).
SQ SEQUENCE 1142 AA; 126871 MW; 425D71B8340B3F8F CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1142;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LINTSDST 29
| | | | |
Db 559 LINTSDST 565

RESULT 56
PYC1_YEAST STANDARD; PRT; 1178 AA.
AC P11154;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase 1 (EC 6.4.1.1) (Pyruvic carboxylase 1) (PCB 1).
GN PYC1 OR PIV OR YGL062W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=82298805; PubMed=3042770;
RA Lim F., Morris C.P., Ochlodoro F., Wallace J.C.;
RT "Sequence and domain structure of yeast pyruvate carboxylase.";
RL J. Biol. Chem. 263:11493-11497 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97377993; PubMed=9234674;

RA Feuermann M., de Montigny J., Potier S., Souciet J.-L.;
RT "The characterization of two new clusters of duplicated genes
RT suggests a 'lego' organization of the yeast Saccharomyces cerevisiae
RT chromosomes.";
RL Yeast 13:861-869 (1997).
RN [3]
RP SEQUENCE OF 1003-1178 FROM N.A.
RX MEDLINE=87241529; PubMed=3036126;
RA Morris C.P., Lim F., Wallace J.C.;
RT "Yeast pyruvate carboxylase: gene isolation.";
RL Biochem. Biophys. Res. Commun. 145:390-396 (1987).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and zinc.
CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J03889; AAA34843.1; -
CC EMBL: Z72584; CAA96765.1; -
CC PIR: S64066; QYBYP.
CC HSP: P24182; IBNC.
CC GerMOnline: 141110; -
CC SGP: S0003030; PYC1.
CC GO: GO:0005829; C:cytosol; IDA.
CC GO: GO:0004736; F:pyruvate carboxylase activity; IDA.
CC InterPro: IPR001882; Biotin_BS.
CC InterPro: IPR005482; Biotin_carb_C.
CC InterPro: IPR000089; Biotin_lipoyl.
CC InterPro: IPR005479; CPase_L_D2.
CC InterPro: IPR005481; CPase_L_N.
CC InterPro: IPR000891; HMGL-Like.
CC InterPro: IPR003379; PYC_OADA.
CC InterPro: IPR005930; Pyruv_carbox.
CC Pfam: PF02785; Biotin_carb_C; 1.
CC Pfam: PF00364; Biotin_lipoyl; 1.
CC Pfam: PF00289; CPase_L_chain; 1.
CC Pfam: PF02786; CPase_L_D2; 1.
CC Pfam: PF00682; HMGL-Like; 1.
CC Pfam: PF02436; PYC_OADA; 1.
CC TIGRfam: TIGR01235; Pyruv_carbox; 1.
CC PROSITE: PS00188; BIOTIN_1.
CC PROSITE: PS00866; CPASE_1; 1.
CC PROSITE: PS00867; CPASE_2; 1.
CC Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
KW Zinc; Multigene family.
FT NP_BIND 182 187 ATP (POTENTIAL).
FT ACT_SITE 312 312 BY SIMILARITY.
FT BINDING 1135 1135 BIOTIN (BY SIMILARITY).
FT CONFLICT 462 462 T -> G (IN REF. 1).
FT CONFLICT 493 493 V -> D (IN REF. 1).
FT CONFLICT 595 595 R -> A (IN REF. 1).
FT CONFLICT 619 619 E -> Q (IN REF. 1).
FT CONFLICT 664 664 G -> S (IN REF. 1).
FT CONFLICT 772 772 A -> R (IN REF. 1).
FT CONFLICT 879 879 E -> Q (IN REF. 1).
FT CONFLICT 909 909 Q -> K (IN REF. 1).
SQ SEQUENCE 1178 AA; 130099 MW; BC7110A8AFB23E04 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1178;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 ETDEIE 395
DB 1033 ETDEIE 1039

RESULT 57
SYJ2 RAT
ID SYJ2 RAT STANDARD; PRT; 1248 AA.
AC 055207;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Synaptotagmin 2 (EC 3.1.3.36) (Synaptic inositol-1,4,5-trisphosphate 5-phosphatase 2).
GN SYJ2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Brain;
RA MEDLINE=98049546; PubMed=9388224;
RX Nemoto Y., Arribas M., Hafner C., de Camilli P.;
RT "Synaptotagmin 2, a novel synaptotagmin isoform with a distinct targeting domain and expression pattern.";
RL EMBO J. 18:2991-3006(1999).
RN [2]
RP FUNCTION: Inositol 3-phosphatase which may be involved in distinct membrane trafficking and signal transduction pathways.
CC -!- CATALYTIC ACTIVITY: 1-phosphatidy-1D-myo-inositol 4,5-bisphosphate + H(2)O = 1-phosphatidyl-1D-myo-inositol 4-phosphate + phosphate.
CC -!- SUBUNIT: Binds to GRB2 (by similarity). Isoform 2A binds to OMP25.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. INTERACTION OF ISOFORM 2A WITH OMP25 RESULTS IN LOCALIZATION TO THE MITOCHONDRIA.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Comment=Additional isoforms seem to exist. Experimental confirmation may be lacking for some isoforms;
CC Name=2A; Synonyms=7.5kb;
CC IsoId=O55207-1; Sequence=Displayed;
CC Name=7.2kb;
CC IsoId=O55207-5; Sequence=Not described;
CC Name=6.0kb;
CC IsoId=O55207-4; Sequence=Not described;
CC Name=5.2kb;
CC IsoId=O55207-3; Sequence=Not described;
CC Name=3.5kb;
CC IsoId=O55207-2; Sequence=Not described;
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: In the central section; belongs to the inositol-1,4,5-trisphosphate 5-phosphatase family.
CC -!- SIMILARITY: Contains 1 SAC domain.
CC -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC
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EMBL; U90312; AAB92481.1; -;
InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR000300; IPR000504; RNA_rec_mot.
InterPro; IPR002013; SYJA_N.
Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF00076; rrm; 1.
DR Pfam; PF02383; SYJA_N; 1.
DR SMART; SM00128; IPEC; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS0030; RRM_RNP_1; FALSE_NEG.
DR PROSITE; PS0275; SAC; 1.
KW Hydrolase; Alternative splicing; RNA-binding; Multigene family.
FT DOMAIN 120 444
FT DOMAIN 450 ?
FT DOMAIN 906 ?
FT DOMAIN 1233 1248
FT DOMAIN 1246 1248
FT MUTAGEN 1248 1248
V->A: ABOLISHES OMP25-BINDING.
S->A: ABOLISHES OMP25-BINDING.
SQ SEQUENCE 1248 AA; 138275 MW; 14E4F3521A4EC1A CRC64;
CATALYTIC (BY SIMILARITY).
BINDS PDZ DOMAIN OF OMP25.
V->A: ABOLISHES OMP25-BINDING.
S->A: ABOLISHES OMP25-BINDING.
SQ SEQUENCE 1248 AA; 138275 MW; 14E4F3521A4EC1A CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1248;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 ALKKILS 90
DB 119 ALKKILS 125

RESULT 58
VG37_BPT2
ID VG37_BPT2 STANDARD; PRT; 1341 AA.
AC P07067;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Long tail fiber protein p37 (Protein Gp37) (Receptor recognizing protein).
GN 37.
OS Bacteriophage T2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10664;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87112716; PubMed=3806672;
RA Riede I., Drexler K., Eschbach M.-L., Henning U.;
RT "DNA sequence of the tail fiber genes 37, encoding the receptor recognizing part of the fiber, of bacteriophages T2 and K3.";
RL J. Mol. Biol. 191:255-266(1986).
CC -!- FUNCTION: Structural component of the distal-half tail fiber.
CC -!- SUBUNIT: The distal half-fiber contains two molecules each of Gp36 and Gp37 and one molecule of Gp35.
CC -!- SIMILARITY: Belongs to the tail fiber family.
CC
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 VVGWYKF 102
Db 820 VVGWYKF 826

RESULT 59
SYJ2_HUMAN
ID SYJ2_HUMAN STANDARD; PRT; 1443 AA.
AC O15056;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Synaptotagmin 2 [EC 3.1.3.36] (Synaptic inositol-1,4,5-trisphosphate 5-
DE phosphatase 2) (Fragment).
GN SYN2 OR KIAA0348.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Nemoto Y., de Camilli P.;
RT "Characterization of an alternative spliced form of synaptotagmin 2.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 331-1443 FROM N.A.
RC TISSUE=Brain;
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 4:141-150(1997).
CC -!- FUNCTION: Inositol 5-phosphatase which may be involved in distinct
CC membrane trafficking and signal transduction pathways.
CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = 1-phosphatidyl-1D-myo-inositol 4-phosphate
CC + phosphate.
CC -!- SUBUNIT: Binds to GRB2.
CC -!- SUBCELLULAR LOCATION: PREDOMINANTLY ASSOCIATED WITH THE
CC PARTICULATE FRACTIONS (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=O15056-1; Sequence-Displayed;
CC -!- DOMAIN: The C-terminal proline-rich region mediates binding only
CC to the SH3 domain-containing protein GRB2.
CC -!- SIMILARITY: In the central section; belongs to the inositol-1,4,5-
CC trisphosphate 5-phosphatase family.
CC -!- SIMILARITY: Contains 1 SAC domain.
CC -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC
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CC
CC EMBL; AF039945; AAD02178.1; -.
CC EMBL; ABC02346; BAA20805.2; -.
CC GenBank; HGNC:11504; SYNJ2.
CC InterPro; IPR005135; Exo_endo_phos.
CC InterPro; IPR000300; IPPC.
CC InterPro; IPR000504; RNA_rec_mot.
CC InterPro; IPR002013; SYJA_N.
CC Pfam; PF03372; Exo_endo_phos; 1.

Pfam: PF02383; SyJa_N; 1.
SMART; SM00128; IPPC; 1.
DR PROSITE; PS00102; RRM; 1.
DR PROSITE; PS00300; RRM_RNP_1; FALSE_NEG.
DR PROSITE; PS0275; SAC; 1.
KW Hydrolase; Alternative splicing; RNA-binding; Multigene family.
FT NON_TER 1
FT DOMAIN 67 391 SAC.
FT DOMAIN 397 ? CATALYTIC (BY SIMILARITY).
FT DOMAIN 836 915 RNA-BINDING (RRM).
FT DOMAIN 1058 1061 POLY-PRO.
SQ SEQUENCE 1443 AA; 159953 MW; 6C5DAE90FCC1B02B CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1443;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 84 ALKKILS 90
Db 66 ALKKILS 72

RESULT 60
UN89_CABEL
ID UN89_CABEL STANDARD; PRT; 6632 AA.
AC O01761; Q17362;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Muscle M-line assembly protein unc-89 (Uncoordinated protein 89).
DE UNC-89 OR C09D1.1.
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.; FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=Bristol N2;
RX MEDLINE=96180278; PubMed=8603916;
RA Benian G.M., Finley T.L., Tang X., Borodovsky M.;
RT "The Caenorhabditis elegans gene unc-89, required for muscle M-line
RT assembly, encodes a giant modular protein composed of 19 and signal
RT transduction domains.";
RL J. Cell Biol. 132:835-848(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Le T.T., Wilson R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Structural component of the muscle M-line. Myofilament
CC lattice assembly begins with positional cues laid down in the
CC basement membrane and muscle cell membrane. UNC-89 responds to
CC these signals, localizes, and then participates in assembling an
CC M-line.
CC -!- TISSUE SPECIFICITY: Localizes to the middle of A-bands.
CC -!- SIMILARITY: Contains 1 DEL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 5 RCDSD domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC
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CC -----
DR EMBL; U33058; AAB00542.1; .
DR EMBL; AF003131; AAB54132.2; -.
DR PDB; 1PHO; 20-DEC-00.
DR WormPep; C09D1.1; CE30426.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; I9-like.
DR InterPro; IPR003598; I9_c2.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR001849; PH.
DR InterPro; IPR007850; RCSD.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 47.
DR Pfam; PF0169; PH; 1.
DR Pfam; PF05177; RCSD; 5.
DR Pfam; PF0621; RhGEF; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00408; IGC2; 23.
DR SMART; SM00325; RhGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS0010; DH 2; 1.
DR PROSITE; PS00835; IG-LIKE; 49.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00002; SH3; 1.
KW Muscle protein; Immunoglobulin domain; Repeat; SH3 domain;
KW 3D-structure.
FT DOMAIN 63 127 SH3.
FT DOMAIN 152 330 DH.
FT DOMAIN 342 498 PH.
FT DOMAIN 547 633 IG-LIKE C2-TYPE 1.
FT DOMAIN 648 736 IG-LIKE C2-TYPE 2.
FT DOMAIN 748 838 IG-LIKE C2-TYPE 3.
FT DOMAIN 946 1033 IG-LIKE C2-TYPE 4.
FT DOMAIN 1044 1132 IG-LIKE C2-TYPE 5.
FT DOMAIN 1140 1227 IG-LIKE C2-TYPE 6.
FT DOMAIN 1272 1315 THR-RICH.
FT DOMAIN 1375 1475 RCSD 1.
FT DOMAIN 1479 1585 RCSD 2.
FT DOMAIN 1597 1695 RCSD 3.
FT DOMAIN 1700 1799 RCSD 4.
FT DOMAIN 1800 1860 RCSD 5.
FT DOMAIN 1982 2067 IG-LIKE C2-TYPE 7.
FT DOMAIN 2071 2163 IG-LIKE C2-TYPE 8.
FT DOMAIN 2171 2261 IG-LIKE C2-TYPE 9.
FT DOMAIN 2269 2359 IG-LIKE C2-TYPE 10.
FT DOMAIN 2367 2455 IG-LIKE C2-TYPE 11.
FT DOMAIN 2463 2564 IG-LIKE C2-TYPE 12.
FT DOMAIN 2563 2651 IG-LIKE C2-TYPE 13.
FT DOMAIN 2657 2746 IG-LIKE C2-TYPE 14.
FT DOMAIN 2754 2858 IG-LIKE C2-TYPE 15.
FT DOMAIN 2887 2980 IG-LIKE C2-TYPE 16.
FT DOMAIN 2994 3081 IG-LIKE C2-TYPE 17.
FT DOMAIN 3087 3183 IG-LIKE C2-TYPE 18.
FT DOMAIN 3189 3280 IG-LIKE C2-TYPE 19.
FT DOMAIN 3286 3376 IG-LIKE C2-TYPE 20.
FT DOMAIN 3384 3469 IG-LIKE C2-TYPE 21.
FT DOMAIN 3482 3572 IG-LIKE C2-TYPE 22.
FT DOMAIN 3580 3667 IG-LIKE C2-TYPE 23.
FT DOMAIN 3686 3777 IG-LIKE C2-TYPE 24.
FT DOMAIN 3817 3908 IG-LIKE C2-TYPE 25.
FT DOMAIN 3920 4009 IG-LIKE C2-TYPE 26.
FT DOMAIN 4018 4106 IG-LIKE C2-TYPE 27.
FT DOMAIN 4109 4201 IG-LIKE C2-TYPE 28.
FT DOMAIN 4212 4297 IG-LIKE C2-TYPE 29.
FT DOMAIN 4302 4387 IG-LIKE C2-TYPE 30.
FT DOMAIN 4400 4485 IG-LIKE C2-TYPE 31.
FT DOMAIN 4489 4580 IG-LIKE C2-TYPE 32.
FT DOMAIN 4588 4678 IG-LIKE C2-TYPE 33.
FT DOMAIN 4681 4771 IG-LIKE C2-TYPE 34.
FT DOMAIN 4873 4961 IG-LIKE C2-TYPE 35.
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FT DOMAIN 4965 5057 IG-LIKE C2-TYPE 36.
FT DOMAIN 5067 5160 IG-LIKE C2-TYPE 37.
FT DOMAIN 5171 5260 IG-LIKE C2-TYPE 38.
FT DOMAIN 5277 5366 IG-LIKE C2-TYPE 39.
FT DOMAIN 5383 5472 IG-LIKE C2-TYPE 40.
FT DOMAIN 5487 5578 IG-LIKE C2-TYPE 41.
FT DOMAIN 5595 5685 IG-LIKE C2-TYPE 42.
FT DOMAIN 5701 5790 IG-LIKE C2-TYPE 43.
FT DOMAIN 5815 5904 IG-LIKE C2-TYPE 44.
FT DOMAIN 5925 6014 IG-LIKE C2-TYPE 45.
FT DOMAIN 6038 6130 IG-LIKE C2-TYPE 46.
FT DOMAIN 6150 6239 IG-LIKE C2-TYPE 47.
FT DOMAIN 6275 6368 FIBRONECTIN TYPE-III.
FT DOMAIN 6413 6502 IG-LIKE C2-TYPE 48.
FT DOMAIN 6507 6596 IG-LIKE C2-TYPE 49.
FT DISULFID 568 621 POTENTIAL.
FT DISULFID 2908 2975 POTENTIAL.
FT DISULFID 3015 3065 POTENTIAL.
FT DISULFID 3707 3759 POTENTIAL.
FT DISULFID 3826 3890 POTENTIAL.
FT DISULFID 5092 5157 POTENTIAL.
FT DISULFID 5298 5350 POTENTIAL.
FT DISULFID 5508 5569 POTENTIAL.
FT DISULFID 5616 5669 POTENTIAL.
FT DISULFID 5722 5764 POTENTIAL.
FT DISULFID 5836 5901 POTENTIAL.
FT DISULFID 5946 5998 POTENTIAL.
FT DISULFID 6036 6171 POTENTIAL.
FT DISULFID 6421 6486 POTENTIAL.
FT CONFLICT 2137 2137 A -> P (IN REF. 1).
FT CONFLICT 2245 2247 AKK -> PKP (IN REF. 1).
FT CONFLICT 2258 2258 A -> P (IN REF. 1).
FT CONFLICT 2284 2284 E -> G (IN REF. 1).
FT CONFLICT 2297 2297 M -> I (IN REF. 1).
FT CONFLICT 3531 3531 A -> G (IN REF. 1).
FT CONFLICT 3884 3888 DAGGY -> RRRI (IN REF. 1).
FT CONFLICT 3929 3929 A -> V (IN REF. 1).
FT CONFLICT 5134 5134 A -> P (IN REF. 1).
FT CONFLICT 5145 5145 T -> S (IN REF. 1).
FT CONFLICT 5185 5185 G -> A (IN REF. 1).
FT CONFLICT 5199 5199 K -> N (IN REF. 1).
FT CONFLICT 5202 5202 L -> F (IN REF. 1).
FT CONFLICT 5213 5213 F -> L (IN REF. 1).
FT CONFLICT 6178 6178 A -> G (IN REF. 1).
FT CONFLICT 6268 6268 K -> E (IN REF. 1).
SQ SEQUENCE 6632 AA; 731665 MW; 262D3EDD62960E89 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 6632;
Best Local Similarity 100.0%; Pred.No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 EEDGSLK 210
Db 2515 EEDGSLK 2521
|||||
EEDGSLK 210
EEDGSLK 2521

RESULT 61
KDPP_ECOLI STANDARD; PRT; 29 AA.
ID KDPP_ECOLI
AC P36937;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kDPP
GN KDPF OR B0698.1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A. PubMed=6146979;
RX MEDLINE=84272710; PubMed=6146979;
Hesse J.E.; Wiczorek L.; Altendorf K.; Reicin A.S.; Dorus E.,
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OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN (1)
RN SEQUENCE FROM N.A.
RP STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Patthugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-F., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd";
RT Science 269:496-512(1995).
CC -----
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CC -----
CC EMBL; U32807; AAC22930.1; -;
DR PIR; D64024; D64024.
DR TIGR; H11269; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 38 AA; 4562 MW; DDF1140F18742BDF CRC64;

Query Match 1.5%; Score 6; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 NEQALK 86
|||
DB 28 NEQALK 33

RESULT 63
TPCS_PROBDO
ID TPCS_PRODO STANDARD; PRT; 52 AA.
AC P81074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Troponin C, skeletal muscle (Fragment).
OS Protoperus dolloi (Slender lungfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Dipnoi; Lepidosireniformes; Protopteridae; Protopterus.
OX NCBI_TaxID=27779;
RN (1)
RN SEQUENCE.
RX MEDLINE=97442870; PubMed=9297801;
RA Francis J.M., Altintas A., Gerday C.;
RT "Characterization of the single tyrosine containing troponin C from
RT lungfish white muscle. Comparison with several fast skeletal muscle
RT troponin C's from fish species.";
RL Comp. Biochem. Physiol. 117B:589-598(1997).
CC -!- FUNCTION: Troponin is the central regulatory protein of striated
CC muscle contraction. It consists of three components: Tn-I which is
CC the inhibitor of actomyosin ATPase, Tn-T which contains the
CC binding site for troponin and Tn-C. The binding of calcium to
CC Tn-C abolishes the inhibitory action of Tn on actin filaments.
CC -!- MISCELLANEOUS: Skeletal muscle troponin C binds four calcium ions.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR HSPF; P02586; IYN4.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD000012; EF-hand; 1.

RL Nature 409:685-690 (2001).
RL "Functional annotation of a full-length mouse cDNA collection.";

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RX MEDLINE=90127394; PubMed=2298292;
RT Terzi E., Boycot P., van Dorsselaer A., Luv B., Trifiliev E.;
RT "Isolation and amino acid sequence of a novel 6.8-kDa mitochondrial
RT proteolipid from beef heart. Use of FAB-MS for molecular mass
RT determination.";
RL FEBS Lett. 260:122-126(1990).
CC -I- SUBCELLULAR LOCATION: Mitochondrial.
CC -I- TISSUE SPECIFICITY: HEART, BRAIN AND LIVER MITOCHONDRIA.
CC -I- MASS SPECTROMETRY: MW=6834.1; METHOD=FAB.
DR PIR; A34138; A34138.
KW Mitochondrion.
SQ SEQUENCE 60 AA; 6834 MW; 0D8AF6566B0AFD12 CRC64;

Query Match 1.5%; Score 6; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 DKRSKA 372
| | | | |
DB 42 DKRSKA 47

RESULT 67
Y766.METJA
ID Y766.METJA STANDARD; PRT; 66 AA.
AC Q58176;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0766.
DE MJ0766.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OC NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RC MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii";
RA Science 273:1058-1073(1996).
RC -I- SIMILARITY: TO M.JANNASCHII MJ0582.

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EMBL; U67522; AAB98773.1; -
DR PIR; F64395; F64395.
DR TIGR; MJ0766; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 66 AA; 7235 MW; A206FD6CB000CCBC CRC64;

Query Match 1.5%; Score 6; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 ERIEKM 397
| | | | |
DB 51 ERIEKM 56

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RESULT 68
Y055 NPVOP          STANDARD;          PRT;      68 AA.
ID   Y055 NPVOP
AC   O10313
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Hypothetical 8.0 kDa protein (ORF59).
OS   Orygia pseudotsugata multicapsid polyhedrosis virus (OpMPV).
OC   Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC   Nucleopolyhedrovirus.
OX   NCBI_TaxID=164623;
RN   [1]
RP   MEDLINE=97271300; PubMed=9126251;
RA   Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
RA   Rohmann G.F.;
RT   "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
RT   polyhedrosis virus genome.";
RL   Virology 229:381-399(1997).
CC   -!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
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CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL: U75930; AAC59058.1; --
KW   Hypothetical protein.
SQ   SEQUENCE 68 AA; 7969 MW; FC2D1C4384AF62C8 CRC64;
      Query Match      1.5%; Score 6; DB 1; Length 68;
      Best Local Similarity 100.0%; Pred. No. 1.3e+02;
      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   240 VDKLVK 245
DB   |||||
      61 VDKLVK 66

RESULT 69
U197 DROME
ID   U197 DROME          STANDARD;          PRT;      78 AA.
AC   Q9VVA8;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypothetical protein CG9669.
GN   CG9669.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.C., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA   Brandon R.G., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

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DR EMBL; U02997; AAB60676.1; -
DR EMBL; U02996; AAB60676.1; JOINED.
DR EMBL; U03028; AA57170.1; -
DR EMBL; U05705; AAB60468.1; -
DR EMBL; U05706; AAB60469.1; -
DR PIR; I48226; I48226.
DR MGD; MGI:94882; Defcr2.
DR InterPro; IPR006081; Defensin alpha.
DR InterPro; IPR006080; Defensin mammal.
DR InterPro; IPR002366; Defensin_propep.
DR Pfam; PF00879; Defensin_propep; 1.
DR Pfam; PF00233; defensins; 1.
DR SMART; SM00048; DEFSN; 1.
DR PROSITE; PS00269; DEFENSIN; 1.
KW Defensin; Antibiotic; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 58
FT CHAIN 59 93 CRYPTDIN-2.
FT DISULFID 64 92 BY SIMILARITY.
FT DISULFID 66 81 BY SIMILARITY.
FT DISULFID 71 91 BY SIMILARITY.
FT CONFLICT 87 87 M -> L (IN REF. 3).
SQ SEQUENCE 93 AA; 10560 MW; 4F05DEA252412B0D CRC64;

Query Match 1.5%; Score 6; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 ASLQEE 225
DB 52 ASLQEE 57

RESULT 73
RM32_SCHPO
ID RM32_SCHPO STANDARD; PRT; 103 AA.
AC Q94379;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable 60S ribosomal protein L32, mitochondrial precursor.
GN SPBC1604.13C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

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RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002)
CC -!- FUNCTION: Component of the large subunit of mitochondrial ribosome
CC (by similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -!- SIMILARITY: Belongs to the L32P family of ribosomal proteins.
CC -----
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CC -----
EMBL; AL034433; CRA22346.1; -
PIR; T39501; T39501.13C; -
GeneDB SPombe; SPBC1604.13C; -
InterPro; IPR002677; Ribosomal L32p.
Pfam; PF01783; Ribosomal L32p; 1.
KW Ribosomal protein; Mitochondrion; Transit peptide.
FT TRANSIT 1 47 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 48 103 PROBABLE 60S RIBOSOMAL PROTEIN L32.
SQ SEQUENCE 103 AA; 11620 MW; 186857894BED688F CRC64;

Query Match 1.5%; Score 6; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 KRSRL 363
DB 59 KRSRL 64

RESULT 74
YIS2_STRCO
ID YIS2_STRCO STANDARD; PRT; 110 AA.
AC P19781;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Insertion element IS110 hypothetical 11.7 kDa protein.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2);
RX MEDLINE=88015544; PubMed=2821490;
RA Bruton C.J., Chater K.F.;
RT "Nucleotide sequence of IS110, an insertion sequence of Streptomyces
coelicolor A3(2).";
RL Nucleic Acids Res. 15:7053-7065(1987).
CC -----
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CC -----
EMBL; Y00434; CAA68493.1; -
PIR; B26848; B26848.
Transposable element; Hypothetical protein.
KW Transposable element; 110 AA; 11745 MW; 8A9D92D2F7514D76 CRC64;
SQ SEQUENCE 110 AA; 11745 MW; 8A9D92D2F7514D76 CRC64;

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Query Match          1.5%; Score 6; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 382 ASKMSS 387
Db 75 ASKMSS 80

RESULT 75
YU44 PYRAE
ID YU44 PYRAE STANDARD; PRT; 110 AA.
AC Q8TX7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein PAE3044.
GN PAE3044.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
CC -!- SIMILARITY: Belongs to the PDCD5 family.
-----
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-----
CC EMBL; AE009908; AAL64632.1; --
DR HAMAP; MF_00026; --; 1.
DR InterPro; IPR002836; TFA19-related.
DR Pfam; PF01984; dsDNA bind; 1.
DR ProDom; PD008148; TFA19-related; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 110 AA; 12925 MW; 6873968F0DD32A35 CRC64;

Query Match          1.5%; Score 6; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 ALKKIL 89
Db 42 ALKKIL 47

RESULT 76
RL30 ORYZA
ID RL30 ORYZA STANDARD; PRT; 111 AA.
AC Q9SDG6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L30.
GN RPL30.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P038F12."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the L30E family of ribosomal proteins.
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-----
CC EMBL; AP000836; BAA88178.1; --
DR HSSP; P14120; ICN9.
DR Gramene; Q9SDG6; --
DR InterPro; IPR000231; Ribosomal L30e.
DR InterPro; IPR004038; Ribosomal L7Ae.
DR Pfam; PF01248; Ribosomal L7Ae; 1.
DR ProDom; PD004495; Ribosomal L30e; 1.
DR PROSITE; PS00709; RIBOSOMAL_L30e_1; 1.
DR PROSITE; PS00993; RIBOSOMAL_L30e_2; 1.
KW Ribosomal protein.
SQ SEQUENCE 111 AA; 12363 MW; 083E7CDE1304C04F CRC64;

Query Match          1.5%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 LGYKTV 182
Db 29 LGYKTV 34

RESULT 77
RL30 EUPES
ID RL30 EUPES STANDARD; PRT; 112 AA.
AC Q9MSN6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L30.
GN RPL30.
OS Euphorbia esula (Leafy spurge).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae; Euphorbiae;
OC Euphorbia.
OX NCBI_TaxID=3993;
RN [1]
RP SEQUENCE FROM N.A.
RA Anderson J.V., Horvath D.P.;
RT "Identification of mRNAs expressed in underground adventitious buds of
RT Euphorbia esula (leafy spurge).";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the L30E family of ribosomal proteins.
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-----
CC EMBL; AF227621; AAF34766.1; --
DR HSSP; P14120; ICN9.
DR InterPro; IPR000231; Ribosomal L30e.
DR InterPro; IPR004038; Ribosomal L7Ae.
DR Pfam; PF01248; Ribosomal L7Ae; 1.

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DR ProDom; PD004495; Ribosomal_L30e; 1.
DR PROSITE; PS00709; RIBOSOMAL_L30E_1; FALSE_NEG.
DR PROSITE; PS00993; RIBOSOMAL_L30E_2; 1.
KW Ribosomal protein.
SQ SEQUENCE 112 AA; 12284 MW; B4018E56AF67E93F CRC64;

Query Match      1.5%; Score 6; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 LGYKTV 182
DB 29 LGYKTV 34

RESULT 78
RL30 LUPLU STANDARD; PRT; 112 AA.
AC O49884;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 60S ribosomal protein L30.
GN RPL30.
OS Lupinus luteus (Yellow lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3873;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ventus; TISSUE=Epicotyl;
RA Nuc P.W., Nuc K.T., Ziolkowski P.A., Slonski R.;
RT "Structure and organization of the yellow lupine ribosomal protein L30
  genes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: Belongs to the L30E family of ribosomal proteins.
CC
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CC
CC EMBL; AJ223316; CAA11256.1; -
CC HSSP; P14120; ICN9.
CC InterPro; IPR000231; Ribosomal_L30e.
CC InterPro; IPR004038; Ribosomal_L7Ae.
CC Pfam; PF01248; Ribosomal_L7Ae; 1.
CC ProDom; PD004495; Ribosomal_L30e; 1.
CC PROSITE; PS00709; RIBOSOMAL_L30E_1; 1.
CC PROSITE; PS00993; RIBOSOMAL_L30E_2; 1.
KW Ribosomal protein.
SQ SEQUENCE 112 AA; 12332 MW; C696CA64824BDE61 CRC64;

Query Match      1.5%; Score 6; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 LGYKTV 182
DB 29 LGYKTV 34

RESULT 79
RL30 MAIZE STANDARD; PRT; 112 AA.
AC O48558;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 60S ribosomal protein L30.
GN RPL30.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Ahluwalia K.K., Baysdorfer C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: Belongs to the L30E family of ribosomal proteins.
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CC
CC EMBL; AF034949; AAB88620.1; -
CC PIR; T01411; T01411.
CC HSSP; P14120; ICN9.
CC InterPro; IPR000231; Ribosomal_L30e.
CC InterPro; IPR004038; Ribosomal_L7Ae.
CC Pfam; PF01248; Ribosomal_L7Ae; 1.
CC ProDom; PD004495; Ribosomal_L30e; 1.
CC PROSITE; PS00709; RIBOSOMAL_L30E_1; 1.
CC PROSITE; PS00993; RIBOSOMAL_L30E_2; 1.
KW Ribosomal protein.
SQ SEQUENCE 112 AA; 12491 MW; 1D9925D10F1A7CB2 CRC64;

Query Match      1.5%; Score 6; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 LGYKTV 182
DB 29 LGYKTV 34

RESULT 80
YJ74 AQUAE STANDARD; PRT; 114 AA.
AC O67784;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_1974.
GN AQ_1974.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujaay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
  aeolicus";
RL Nature 392:353-358 (1998).
CC
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CC EMBL; AE000766; AAC07755.1; -
DR PIR; D70469; D70469.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 114 AA; 13914 MW; 0561DBF858B8DF2 CRC64;

Query Match
Best Local Similarity 100.0%; DB 1; Length 114;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LKILLS 90
DB 2 LKILLS 7

RESULT 81
NU3M_SQUAC STANDARD; PRT; 116 AA.
ID Q9Z247;
AC Q9Z247;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3).
GN MTND3 OR ND3
OS Squalus acanthias (Spiny dogfish).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidae; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99091711; PubMed=9873084;
RA Raemussen A.S.; Arnason U.;
RT "Phylogenetic studies of complete mitochondrial DNA molecules place
RT cartilaginous fishes within the tree of bony fishes.";
RL J. Mol. Evol. 48:118-123(1999).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SIMILARITY: Belongs to the complex I subunit 3 family.
CC
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CC
CC EMBL; Y18134; CAA77056.1; -
DR PIR; T11541; T11541.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; oxidored_q4; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 116 AA; 12907 MW; 5A87A2557435793F CRC64;

Query Match
Best Local Similarity 100.0%; DB 1; Length 116;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 LLTPSI 139
DB 82 LLTPSI 87

RESULT 82
AMC2_PIG STANDARD; PRT; 117 AA.
ID AMC2_PIG
AC P22952;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alveolar macrophage chemotactic factor II precursor (AMCF-II).
DS Sus scrofa (Pig).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 37-66.
RX TISSUE=Lung;
MEDLINE=93041741; PubMed=1420165;
RA Goodman R.B.; Foster D.C.; Mathewes S.L.; Osborn S.G.; Kuijper J.L.;
RA Forstrom J.W.; Martin T.R.;
RT "Molecular cloning of porcine alveolar macrophage-derived neutrophil
RT chemotactic factors I and II; identification of porcine IL-8 and
RT another intercrine-alpha protein.";
RL Biochemistry 31:10483-10490(1992).
RN [2]
RP SEQUENCE OF 37-66.
RX STRAIN=Yorkshire;
MEDLINE=91217086; PubMed=1850745;
RA Goodman R.B.; Forstrom J.W.; Osborn S.G.; Chi E.Y.; Martin T.R.;
RT "Identification of two neutrophil chemotactic peptides produced by
RT porcine alveolar macrophages.";
RL J. Biol. Chem. 266:8455-8463(1991).
CC -!- FUNCTION: Has chemotactic activity for porcine, and in a lesser
CC extent, for human neutrophils.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Alveolar macrophages.
CC -!- INDUCTION: By lipopolysaccharide (LPS).
CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokines Cx-C)
CC family.
CC
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CC
CC EMBL; M99368; AAA30991.1; -
DR PIR; B39819; B39819.
DR PIR; B44253; B44253.
DR HSPSP; P02775; INAP.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXCL12; CXCL12.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTCKXC.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 36
FT CHAIN 37 117 ALVEOLAR MACROPHAGE CHEMOTACTIC FACTOR
FT II.
FT BY SIMILARITY.
FT DISULFID 52 78
FT DISULFID 54 94 BY SIMILARITY.
SQ SEQUENCE 117 AA; 12343 MW; CD3D27410934F910 CRC64;

Query Match
Best Local Similarity 100.0%; DB 1; Length 117;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 LLTPSI 138
DB 25 LLTPSI 30

RESULT 83
YE55_PVRHO STANDARD; PRT; 120 AA.
ID YE55_PVRHO
AC G59124;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein PH1455.
GN PH1455.
OS Pyrococcus horikoshii.

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OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -!- SIMILARITY: Belongs to the UPF0091 family.
CC
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CC
CC EMBL; AP000006; BAA30562.1; -.
DR PIR; B71020; B71020.
DR InterPro; IPR005133; Pfam; Mnhg_YufB.
DR Pfam; PF03334; Pfam; Mnhg_YufB; 1.
DR TIGRFAMs; TIGR01300; CPA3_mnhg_phaG; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 120 AA; 13088 MW; B3E8730F741FB872 CRC64;

Query Match 1.5%; Score 6; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VFLLLT 136
DB 76 VFLLLT 81

RESULT 84
ZEAV MAIZE
ID ZEAV MAIZE STANDARD; PRT; 122 AA.
AC P05615.
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE Zein-alpha (22 kDa) (Clone B49) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84207881; PubMed=6897917;
RA Geraghty D.E., Messing J., Rubenstein I.;
RT "Sequence analysis and comparison of cDNAs of the zein multigene
RT family.";
RL EMBO J. 1:1329-1335(1982).
CC -!- FUNCTION: Zeins are major seed storage proteins.
CC -!- MISCELLANEOUS: The alpha zeins of 19 kDa and 22 kDa account for
CC 70% of the total zein fraction. They are encoded by a large
CC multigene family.
CC -!- MISCELLANEOUS: STRUCTURALLY, 22K AND 19K ZEINS ARE COMPOSED OF
CC NINE ADJACENT, TOPOLOGICALLY ANTIPARALLEL HELICES CLUSTERED WITHIN
CC A DISTORTED CYLINDER.
DR PIR; B22762; Z1ZM49.
DR MaizeDB; 58096; -.
DR InterPro; IPR002530; Zein.
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DR Pfam; PF01559; Zein; 1.
KW Seed storage protein; Repeat; Multigene family.
FT NON_TER 1
SQ SEQUENCE 122 AA; 13424 MW; CADF45F2A3F08A7A CRC64;

Query Match 1.5%; Score 6; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 PLVVAN 170
DB 80 PLVVAN 85

RESULT 85
PFDB HALN1
ID PFDB HALN1 STANDARD; PRT; 125 AA.
AC Q9HSH0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prefoldin beta subunit (GimC beta subunit).
GN PFDB OR VNG0234C.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
RA Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jabloncki P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Beck R.P., Pohlshroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Oner A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -!- FUNCTION: Molecular chaperone capable of stabilizing a range of
CC proteins. Seems to fulfil an ATP-independent, HSP70-like function
CC in archaeal de novo protein folding (By similarity).
CC -!- SUBUNIT: Heterohexamer of two alpha and four beta subunits (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the prefoldin beta subunit family.
CC
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CC
CC EMBL; AB004987; AGL18836.1; -.
DR PIR; H84183; H84183.
DR HAMAP; MF_00307; -.
DR InterPro; IPR002777; PrefoldinKE2.
DR Pfam; PF01920; KE2; 1.
KW Chaperone; Complete proteome.
SQ SEQUENCE 125 AA; 13806 MW; C22F651653A8917F CRC64;

Query Match 1.5%; Score 6; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEEL 226
DB 103 SLOEEL 108
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RESULT 86
Y576 HAEIN STANDARD; PRT; 126 AA.
ID Y576 HAEIN STANDARD; PRT; 126 AA.
AC P44762;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H10576.
GN H10576.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RA MEDLINE=95350630; PubMed=7542800;
RA Fleischnann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kexlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RD."
RL Science 269:496-512(1995).
CC -1- SIMILARITY: Belongs to the UPF0163 (dsrE) family.
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CC
CC EMBL; U32739; AAC22234.1; -.
CC PIR; C64155; C64155.
CC TIGR; H10576; -.
CC HAMAP; MF_00390; -. 1.
CC InterPro; IPR003787; DsrE.
CC Pfam; PF02635; DsrE; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 126 AA; 13997 MW; A237D65A4C46D011 CRC64;
Query Match 1.5%; Score 6; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 319 VVDNLT 324
DB 87 VVDNLT 92
|||||
RESULT 87
YB01 PASMU STANDARD; PRT; 126 AA.
ID YB01 PASMU STANDARD; PRT; 126 AA.
AC Q9CLV1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein PM1101.
GN PM1101.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RL May B.J., Zhang Q., Li L.L., Raustian M.L., Whittam T.S., Kapur V.;
RL "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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CC
CC EMBL; AB006151; AAK03185.1; -.
CC XN Hypothetical protein; Transmembrane; Complete proteome.
CC FT TRANSMEM 40 57 Potential.
CC FT TRANSMEM 72 94 Potential.
CC SQ SEQUENCE 126 AA; 14092 MW; E27FA8E31D51DB46 CRC64;
Query Match 1.5%; Score 6; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 LGALAF 20
DB 45 LGALAF 50
|||||
RESULT 88
RS11 NITEU STANDARD; PRT; 129 AA.
ID RS11 NITEU STANDARD; PRT; 129 AA.
AC Q82X71;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S11.
DE RPSK OR NE0424.
GN Nitrosomonas europaea.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.S., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Holmes N.G., Whittaker M.M., Arp D.J.;
RA "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
CC -1- FUNCTION: Located on the platform of the 30S subunit, it bridges
CC several disparate RNA helices of the 16S rRNA. Forms part of the
CC Shine-Dalgarno cleft in the 70S ribosome (By similarity).
CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Interacts with
CC proteins S7 and S18. Binds to IF-3 (By similarity).
CC -1- SIMILARITY: Belongs to the S11P family of ribosomal proteins.
CC
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CC
CC EMBL; BX321857; CAD84335.1; -.
CC HAMAP; MF_01310; -. 1.
CC InterPro; IPR001971; Ribosomal_S11.
CC Pfam; PF00411; Ribosomal_S11; 1.
CC ProDom; PD001010; Ribosomal_S11; 1.
CC PROSITE; PS00054; Ribosomal_S11; 1.
CC Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
KW
```

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SQ SEQUENCE 129 AA; 13750 MW; E6827A2D1E2FC8C9 CRC64;
Query Match 1.5%; Score 6; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 VKKNV 97
DB 12 VKKNV 17

RESULT 89
V132 FOWPV STANDARD; PRT; 129 AA.
AC P15914;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein FV132.
GN FV132 OR FP6.
OS Fowlpox virus (FPV).
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OC NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FP-9 / Isolate HP-444;
RX MEDLINE=88258470; PubMed=2938574;
RA Binns M.M., Tomley F.M., Campbell J., Boursnell M.E.G.;
RT "Comparison of a conserved region in fowlpox virus and vaccinia virus
RT genomes and the translocation of the fowlpox virus thymidine kinase
RT gene.";
RL J. Gen. Virol. 69:1275-1283 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Salisbury;
RX MEDLINE=87321104; PubMed=2820129;
RA Drillien R., Spehner D., Villevall D., Lecocq J.P.;
RT "Similar genetic organization between a region of fowlpox virus DNA
RT and the vaccinia virus HindIII J fragment despite divergent location
RT of the thymidine kinase gene.";
RL Virol. 74:3815-3831 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Afonso C.L., Tulman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831 (2000).
CC -!- SIMILARITY: Belongs to the poxviruses L5 family.
CC
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CC
CC ENBL; D00320; BAA00229.1; -
CC ENBL; M17418; AAA66420.1; -
CC ENBL; AF198100; AAF44476.1; -
CC PIR; JS0226; WMVZP6.
CC InterPro; IPR006956; Pox L5.
CC Pfam; PF04872; Pox L5; 1
CC SEQUENCE 129 AA; 14745 MW; DB98CC282E48A6B CRC64;

Query Match 1.5%; Score 6; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 EEDGSL 209
DB 77 EEDGSL 82

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RESULT 90
YN09 YEAST STANDARD; PRT; 131 AA.
AC P53841;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 15.3 kDa protein in ALP1-LYP1 intergenic region.
GN YNL269W OR N0670.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96310631; PubMed=8740425;
RA Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.;
RT "The sequence of a 24,152 bp segment from the left arm of chromosome
RT XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
RT genes.";
RL Yeast 12:505-514 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96310631; PubMed=8740425;
RA Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.;
RT "The sequence of a 24,152 bp segment from the left arm of chromosome
RT XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
RT genes.";
RL Yeast 12:505-514 (1996).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; X92494; CAA63229.1; -
CC ENBL; Z71545; CAA96176.1; -
CC PIR; S60913; S60913.
CC Germonline; 143275; -
CC SGD; S0005213; YNL269W.
CC Hypothetical protein.
CC SEQUENCE 131 AA; 15314 MW; F9B0C290CB317B8C CRC64;

Query Match 1.5%; Score 6; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 FLCQAL 284
DB 75 FLCQAL 80

RESULT 91
RUVX HELPY STANDARD; PRT; 134 AA.
AC O2510L;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative Holliday junction resolvase (BC 3.1.-.-).
GN HP0334.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OC NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

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RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
CC -1- FUNCTION: Could be a nuclease that resolves Holliday junction
CC intermediates in genetic recombination.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the YqgF_HRP family.
CC
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CC
CC EMBL; AE000551; AAD07403.1; -;
CC PIR; F64561; P64561.
CC TIGR; H90334; -;
CC HAMAP; MF_00651; -; 1.
CC InterPro; IPR005227; Cons hypoch250.
CC InterPro; IPR006641; YqgFC.
CC Pfam; PF03652; UPF0081; 1.
CC SMART; SM00732; YqgFC; 1.
CC TIGRFAMs; TIGR00250; TIGR00250; 1.
CC Hydrolase; Nuclease; DNA repair; DNA recombination; Complete proteome.
KW
SQ SEQUENCE 134 AA; 15256 MW; 516D8C4233B932CE CRC64;

Query Match 1.5%; Score 6; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 REKNIQ 271
Db 45 REKNIQ 50

RESULT 92
C17_HUMAN STANDARD; PRT; 136 AA.
AC Q9NR1; -;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytokine-like protein C17 precursor.
GN C4ORF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RC TISSUE=Blood;
RX MEDLINE=20313895; PubMed=10857752;
RA Liu X., Rapp N., Deans R., Cheng L.;
RT "Molecular cloning and chromosomal mapping of a candidate cytokine
RT gene selectively expressed in human CD34+ cells.";
RL Genomics 65:283-292(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Specifically expressed in CD34+ hematopoietic
CC cells.
CC
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CC
CC EMBL; AF193766; AA73372.1; -;
CC EMBL; BC031391; AAH31391.1; -;
CC MIM; 607930; -;
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 136 CYTOKINE-LIKE PROTEIN C17.
SQ SEQUENCE 136 AA; 15577 MW; 1CABE1BFC31A3AE3 CRC84;

Query Match 1.5%; Score 6; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFL 134
Db 110 DLVFL 115

RESULT 93
MSCL_PSEFL STANDARD; PRT; 136 AA.
ID MSCL_PSEFL
AC O68286; -;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Large-conductance mechanosensitive channel.
GN MSCL
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98294049; PubMed=9632260;
RA Moe P.C., Slout P., Kung C.;
RT "Functional and structural conservation in the mechanosensitive
RT channel mscl implicates elements crucial for mechanosensation.";
RL Mol. Microbiol. 28:583-592(1998).
CC -1- FUNCTION: Channel that opens in response to stretch forces in the
CC membrane lipid bilayer. May participate in the regulation of
CC osmotic pressure changes within the cell.
CC -1- SUBUNIT: Homopentamer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- SIMILARITY: Belongs to the mscl family.
CC
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CC EMBL; AF029732; AAC38561.1; -
CC HSP; O53898; LMSL; -; 1.
CC HAMAP; MF_00115; -; 1.
CC InterPro; IPR001185; MS_channel.
CC Pfam; PF01741; MSCL; 1.
CC PRINTS; PR01264; MECHCHANNEL.
CC ProDom; PD007253; MS_channel; 1.
CC TIGRFAMs; TIGR00220; mscl; 1.
CC PROSITE; PS01327; MSCL; 1.
CC Ionic channel; Transmembrane; Inner membrane.
KW DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 16 42 BY SIMILARITY.
FT DOMAIN 43 73 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 74 95 BY SIMILARITY.
FT DOMAIN 96 136 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 136 AA; 14459 MW; 99DACA716E481095 CRC64;

Query Match 1.5%; Score 6; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 NRLKRE 253
Db 99 NRLKRE 104
|||||

RESULT 94
MSCL_PSEAB
ID MSCL_PSEAB STANDARD; PRT; 137 AA.
AC Q9HVH7.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Large-conductance mechanosensitive channel.
GN MSCL OR PA4614.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Huftagie W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Tolentino E., Kas A., Larbig K., Lim R.M.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: Channel that opens in response to stretch forces in the
CC membrane lipid bilayer. May participate in the regulation of
CC osmotic pressure changes within the cell (By similarity).
CC -!- SUBUNIT: Homopentamer (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: Belongs to the mscl family.

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CC EMBL; AE004875; AAG08002.1; -
CC PIR; F83069; F83069.
CC HAMAP; MF_00115; -; 1.
CC InterPro; IPR001185; MS_channel.
CC Pfam; PF01741; MSCL; 1.
CC PRINTS; PR01264; MECHCHANNEL.
CC ProDom; PD007253; MS_channel; 1.
CC TIGRFAMs; TIGR00220; mscl; 1.
CC PROSITE; PS01327; MSCL; 1.
CC Ionic channel; Transmembrane; Inner membrane; Complete proteome.
KW DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 16 42 BY SIMILARITY.
FT DOMAIN 43 74 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 75 96 BY SIMILARITY.
FT DOMAIN 97 137 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 137 AA; 14432 MW; FFC0D2A712813BE2 CRC64;

Query Match 1.5%; Score 6; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 NRLKRE 253
Db 100 NRLKRE 105
|||||

RESULT 95
UVSY_BPT4
ID UVSY_BPT4 STANDARD; PRT; 137 AA.
AC P04537;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Recombination protein uvvy.
GN UVSY.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91335767; PubMed=1871975;
RA Gruidl M.E., Chen T.C., Gargano S., Storlazzi A., Cascino A.,
RA Mosig G.;
RT "Two bacteriophage T4 base plate genes (25 and 26) and the DNA repair
RT gene uvvy belong to spatially and temporally overlapping
RT transcription units";
RL Virology 184:359-369(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88319987; PubMed=3412904;
RA Kobayashi M., Saito H., Takahashi H.;
RT "Confirmation of the reading frame of bacteriophage T4 uvvy gene";
RL Nucleic Acids Res. 16:7729-7729(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86072089; PubMed=3000071;
RA Takahashi H., Kobayashi M., Noguchi T., Saito H.;
RT "Nucleotide sequence of bacteriophage T4 uvvy gene";
RL Virology 147:349-353(1985).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87106763; PubMed=3026891;
RA Gruidl M.E., Mosig G.;
RT "Sequence and transcripts of the bacteriophage T4 DNA repair gene
RT uvvy";
RL Genetics 114:1061-1079(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22514363; PubMed=12626685;
RA Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome";

RL Microbiol. Mol. Biol. Rev. 67:86-156(2003).
CC -!- FUNCTION: This protein is involved in the DNA synthesis and
CC recombination process.
CC -----
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CC -----
CC EMBL; M77695; AAA32550.1; -;
CC EMBL; M11495; AAA32546.1; ALT_SEQ.
CC EMBL; X05134; CAA28779.1; -;
CC EMBL; X04856; CAA28549.1; -;
CC EMBL; AF158101; AAD42670.2; -;
CC PIR; J90136; ZXBPT4.
CC DNA synthesis; DNA recombination.
CC CONFLICT 113 113 A -> R (IN REF. 1).
CC SEQUENCE 137 AA; 15839 MW; 63B7A96AA7C3E66 CRC64;
CC
CC Query Match 1.5%; Score 6; DB 1; Length 137;
CC Best Local Similarity 100.0%; Pred. No. 2.3e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 222 LQELK 227
CC
CC DB 6 LQELK 11
CC
CC RESULT 96
CC ATPE SYNPL
CC ID ATPE SYNPL STANDARD; PRT; 138 AA.
CC AC Q05375;
CC DT 01-FEB-1994 (Rel. 28, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE ATP synthase epsilon chain (EC 3.6.3.14) (ATP synthase F1 sector
CC DE epsilon subunit).
CC ATPC OR ATPE.
CC GN Synecococcus sp. (strain PCC 6716).
CC OS Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
CC OX NCBI_TaxID=32048;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=93371369; PubMed=8163578;
CC RA van Walraven H.S., Lutter R., Walker J.E.;
CC RT "Organization and sequences of genes for the subunits of ATP synthase
CC in the thermophilic cyanobacterium Synecococcus 6716.";
CC RL Biochem. J. 294:239-251(1993).
CC CC -!- FUNCTION: Produces ATP from ADP in the presence of a proton
CC CC gradient across the membrane.
CC CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
CC CC H(+) (out)
CC CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC CC core - and CF(0) - the membrane proton channel. CF(1) has five
CC CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
CC CC has three main subunits: a, b and c.
CC CC -!- SIMILARITY: Belongs to the ATPase epsilon chain family.
CC CC -----
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CC -----
CC EMBL; X70432; CAA9883.1; -;
CC HSSP; P00832; IBSN.
CC HAMAP; MF_00530; -; 1.
CC InterPro; IPR001469; ATPsynth_DE.

DR Pfam; PF00401; ATP-synt_DE; 1.
DR Pfam; PF02823; ATP-synt_DE_N; 1.
DR ProDom; PD000944; ATPsynt_DE; 1.
DR TIGRfam; TIGR01216; ATP_synt_eps; 1.
KW Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport.
SQ SEQUENCE 138 AA; 14752 MW; 2EC6F20819C9E17A CRC64;
CC
CC Query Match 1.5%; Score 6; DB 1; Length 138;
CC Best Local Similarity 100.0%; Pred. No. 2.3e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 260 AQIQAA 265
CC
CC DB 114 AQIQAA 119
CC
CC RESULT 97
CC EXD1 VIBCH
CC ID EXD1 VIBCH STANDARD; PRT; 138 AA.
CC AC Q52044; Q9JFZ2;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Biopolymer transport exbd1 protein.
CC GN EXBD1 OR EXBD OR VCA0912.
CC OS Vibrio cholerae.
CC OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
CC OX Vibrionaceae; Vibrio.
CC OX NCBI_TaxID=566;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Classical CA401;
CC RX MEDLINE=98453146; PubMed=9781885;
CC RA Occhino D.A., Wyckoff E.E., Henderson D.P., Wrona T.J., Payne S.M.;
CC RT "Vibrio cholerae iron transport: haem transport genes are linked to
CC one of two sets of tonB, exbB, exbD genes.";
CC RL Mol. Microbiol. 29:1493-1507(1998).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=El Tor N16961 / Serotype O1;
CC RX MEDLINE=20406833; PubMed=10952301;
CC RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
CC RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
CC RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
CC RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
CC RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
CC RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
CC RA Fraser C.M.;
CC RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
CC cholerae.";
CC RL Nature 406:477-483(2000).
CC CC -!- FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT
CC CC TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).
CC CC -!- SUBUNIT: The accessory proteins exbB and exbD seem to form a
CC CC complex with tonB (By similarity).
CC CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
CC CC (Probable).
CC CC -!- SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.
CC CC -----
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CC -----
CC EMBL; AF016580; AAB94546.1; -;
CC EMBL; AE004419; AAF96809.1; -;
CC PIR; D82400; D82400.
CC TIGR; VCA0912; -;
CC InterPro; IPR003400; Exbd.
CC Pfam; PF02472; Exbd; 1.

```
KW Transport; Protein transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 17 37 POTENTIAL.
FT DOMAIN 38 138 PERIPLASMIC (POTENTIAL).
SQ SEQUENCE 138 AA; 15238 MW; E004184FA9C6A3F3 CRC64;

Query Match 1.5%; Score 6; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VFLLLT 136
DB 29 VFLLLT 34

RESULT 98
NIKR PYRHO
ID NIKR PYRHO STANDARD; PRT; 138 AA.
AC O58316,
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Putative nickel responsive regulator.
GN PH0601.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=988344137; PubMed=9679194;
RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hoshoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
CC -!- FUNCTION: Transcriptional regulator (Potential).
CC -!- COFACTOR: Binds 1 nickel ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the copG/nikR family of transcriptional
regulators.
CC
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CC
CC EMBL; AF000002; BAA29690.1; -.
CC FIR; E71175; E71175.
CC HAMAP; MF 00476; -.
CC InterPro; IPR002145; HTH_CopG.
CC Pfam; PF01402; HTH 4; 1.
KW Hypothetical protein; Transcription regulation; DNA-binding; Nickel;
FT METAL 78 78 NICKEL (BY SIMILARITY).
FT METAL 89 89 NICKEL (BY SIMILARITY).
FT METAL 91 91 NICKEL (BY SIMILARITY).
FT METAL 97 97 NICKEL (BY SIMILARITY).
SQ SEQUENCE 138 AA; 15806 MW; A4B8715636C019FE CRC64;

Query Match 1.5%; Score 6; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 VKGEAK 42

Db 103 VKGEAK 108

RESULT 99
Y337 MYCGE
ID Y337 MYCGE STANDARD; PRT; 138 AA.
AC P47579; Q49514;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG337.
GN MG337.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-P., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 52-138 FROM N.A.
RX STRAIN=ATCC 33530 / G-37;
MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
sequencing."
RL J. Bacteriol. 175:7918-7930(1993).
CC
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CC
CC EMBL; U39715; AAC71562.1; -.
CC FIR; U01709; AAB01021.1; -.
CC TIGR; MG337; -.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 52 56 ITAIG -> NYCNW (IN REF. 2).
SQ SEQUENCE 138 AA; 15720 MW; D993716EC6298CE8 CRC64;

Query Match 1.5%; Score 6; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 LLLTPS 138
DB 124 LLLTPS 129

RESULT 100
YORI CALSR
ID YORI CALSR STANDARD; PRT; 140 AA.
AC P40979;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein in xylR 5' region (ORF1) (Fragment).
OS Caldicellulosiruptor sp. (strain R58.4)
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
OC Caldicellulosiruptor.
```



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OX NCBI_TaxID=28238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97077616; PubMed=8920183;
RA Dwivedi P.P., Gibbs M.D., Saul D.J., Bergquist P.L.;
RT "Cloning, sequencing and overexpression in Escherichia coli of a
RT xylanase gene, xynA, from the thermophilic bacterium RtAB.4 genus
RT Caldicellulosiruptor.",
RL Appl. Microbiol. Biotechnol. 45:86-93(1996).
CC -!- FUNCTION: MAY PLAY A ROLE IN SUGAR TRANSPORT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family. MafPG subfamily.
CC -----
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CC -----
DR EMBL; L18965; AAB42041.1; -.
DR PIR; S41785;
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp; 1.
DR PROSITE; PS0928; ABC_TM1; 1.
KW Hypothetical protein; Transmembrane; Transport.
FT NON_TER 1
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 65 85 POTENTIAL.
FT TRANSMEM 115 135 POTENTIAL.
SQ SEQUENCE 140 AA; 15761 MW; FAD18780D9262BF CRC64;

Query Match 1.5%; Score 6; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 LITPSI 139
Db 58 LITPSI 63

Search completed: April 16, 2004, 10:19:27
Job time : 31 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:16:36 ; Search time 21 Seconds
(without alignments)
1873.444 Million cell updates/sec

Title: US-10-063-523-22

Perfect score:

Sequence: 1 MEGESTSAVLSGFVLGALAF.....TDEEIEKMKGFGEYSRSPTF 409

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : PIR 78:*

1: pir1:*

$$p_{112}^* = 0$$

3: p1r3: *

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	9	2.2	546	2	A69484	hypothetical prote
2	8	2.0	246	2	AI3522	taurine transport
3	8	2.0	297	2	F87610	hypothetical prote
4	4	2.0	312	2	T40912	probable lectin pr
5	8	2.0	442	2	AG3924	RNA modification
6	8	2.0	442	2	F97698	probable thiophene
7	8	2.0	470	2	T45272	hypothetical prote
8	8	2.0	613	2	T43738	dnak-type molecula
9	8	2.0	613	2	AE1621	class I heat-shock
10	8	2.0	613	2	AI1258	class I heat-shock
11	8	2.0	1226	2	IS1617	kinesin-like prote
12	7	1.7	92	2	D83736	hypothetical prote
13	7	1.7	104	2	S00120	hypothetical prote
14	7	1.7	104	2	AC0044	probable chaperone
15	7	1.7	105	2	AE1046	SAGE protein limpo
16	7	1.7	136	2	B95086	hypothetical prote
17	7	1.7	136	2	AE1379	hypothetical prote
18	7	1.7	140	2	T26693	hypothetical prote
19	7	1.7	153	2	AB2617	nitrogen regulator
20	7	1.7	153	2	B97399	nitrogen regulator
21	7	1.7	154	2	AD3475	protein-Npi-phosph
22	7	1.7	157	2	H70004	conserved hypophet
23	7	1.7	165	2	S64213	hypothetical prote
24	7	1.7	173	2	E90621	NADH dehydrogenase
25	7	1.7	174	2	E90617	NADH dehydrogenase
26	7	1.7	177	2	T37444	probable 20.7K pro
27	7	1.7	182	2	QJ1801	B7R 21.3K protein
28	7	1.7	185	2	T00519	proline-rich prote
29	7	1.7	187	2	T09390	21K protein precur

30	7	1.7	190	2	G84018	hypothetical prote
31	7	1.7	202	2	T18495	hypothetical prote
32	7	1.7	216	1	B64357	hypothetical prote
33	7	1.7	228	2	T22259	hypothetical prote
34	7	1.7	237	2	H84119	ATP synthase subun
35	7	1.7	254	2	H97081	proline/glycine be
36	7	1.7	256	2	B69197	conserved hypothet
37	7	1.7	257	2	D96161	hypothetical prote
38	7	1.7	266	2	A80024	peptidylprolyl iso
39	7	1.7	266	2	H95122	ABC-2 transporter,
40	7	1.7	282	2	D64456	protein-export mem
41	7	1.7	285	2	T51837	MTN3 homolog [imp
42	7	1.7	294	1	A37818	osteopontin precu
43	7	1.7	296	2	H70208	outer surface prot
44	7	1.7	296	2	S06915	outer surface prot
45	7	1.7	296	2	I40260	outer surface prot
46	7	1.7	296	2	I40258	outer surface prot
47	7	1.7	296	2	I40252	outer surface prot
48	7	1.7	296	2	I40264	outer surface prot
49	7	1.7	296	2	I40250	outer surface prot
50	7	1.7	296	2	I40256	outer surface prot
51	7	1.7	304	2	G84345	hypothetical prote
52	7	1.7	322	2	F90487	maltose ABC transp
53	7	1.7	331	2	G84115	ribose operon tran
54	7	1.7	351	2	T12728	structural protein
55	7	1.7	361	2	I17751	hypothetical prote
56	7	1.7	363	2	JC4748	polygalacturonase
57	7	1.7	378	2	T32526	hypothetical prote
58	7	1.7	385	2	T11892	NADH2 dehydrogen
59	7	1.7	385	2	A86227	hypothetical prote
60	7	1.7	386	2	F70231	conserved hypochet
61	7	1.7	393	2	T06997	2-keto-3-deoxygluc
62	7	1.7	398	2	J00113	hypothetical prote
63	7	1.7	404	2	C71558	probable O-antigen
64	7	1.7	410	2	A80051	hypothetical prote
65	7	1.7	413	2	G70439	hypothetical prote
66	7	1.7	432	2	F81320	transcription term
67	7	1.7	436	2	A11015	probable exported
68	7	1.7	437	2	G82777	glutamate export
69	7	1.7	463	2	T21042	hypothetical prote
70	7	1.7	471	2	A86465	hypothetical prote
71	7	1.7	475	1	A56824	dihydrolipoamide d
72	7	1.7	475	2	T37480	hypothetical prote
73	7	1.7	478	2	S21669	GCD10 protein - ye
74	7	1.7	480	2	F81220	NADH2 dehydrogen
75	7	1.7	481	2	G81796	NADH2 dehydrogen
76	7	1.7	483	2	F71210	hypothetical prote
77	7	1.7	490	2	F89933	hypothetical prote
78	7	1.7	491	2	A28582	tyrosine 3-monooxy
79	7	1.7	498	2	T16417	hypothetical prote
80	7	1.7	506	2	D82081	UDP-N-acetylmuram
81	7	1.7	536	2	T01870	probable pectinest
82	7	1.7	540	2	T04683	precorrin methylas
83	7	1.7	562	2	F72268	ABC transporter, A
84	7	1.7	572	2	F82595	glutathione-regula
85	7	1.7	583	2	AD2395	ATP-binding protei
86	7	1.7	589	2	AC2594	hypothetical prote
87	7	1.7	589	2	E97376	sulfite reductase
88	7	1.7	608	2	S28036	penicillin-binding
89	7	1.7	617	2	G70039	conserved hypothet
90	7	1.7	632	2	H69550	asparagine synthet
91	7	1.7	651	2	D72605	probable long-chain
92	7	1.7	689	2	B82954	conserved hypothet
93	7	1.7	689	2	B69135	coenzyme F420-redu
94	7	1.7	727	2	T18665	hypothetical prote
95	7	1.7	728	2	B71009	hypothetical prote
96	7	1.7	764	2	T05409	hypothetical prote
97	7	1.7	767	2	I51083	SOX-LZ - rainbow t
98	7	1.7	780	2	T27941	hypothetical prote
99	7	1.7	781	2	S51592	XynB precursor - R
100	7	1.7	784	2	G95112	exoribonuclease, R
101	7	1.7	784	2	F97981	exoribonuclease R
102	7	1.7	785	2	T01541	hypothetical prote

103	7	1.7	811	2	E96791	hypothetical prote	176	6	1.5	124	2	S72681	probable membrane
104	7	1.7	860	2	T28227	ORF MSV067 probabl	177	6	1.5	125	2	H94183	hypothetical prote
105	7	1.7	864	2	T01393	apoptosis inhibito	178	6	1.5	125	2	AG2064	hypothetical prote
106	7	1.7	869	2	A88710	protein C43G2.2 [i	179	6	1.5	126	2	C54155	hypothetical prote
107	7	1.7	878	2	T26402	hypothetical prote	180	6	1.5	126	2	AI1951	hypothetical prote
108	7	1.7	908	1	S61476	endopeptidase Clp	181	6	1.5	127	2	A81175	hypothetical prote
109	7	1.7	954	1	S68178	mixed-lineage prot	182	6	1.5	128	4	S59275	hypothetical prote
110	7	1.7	973	2	T00971	transposase tupa -	183	6	1.5	129	1	WMVZP6	F6 protein - fowlp
111	7	1.7	1087	2	T30330	gelsolin-related p	184	6	1.5	130	2	AD2175	two-component resp
112	7	1.7	1142	2	S50632	protein kinase PAK	185	6	1.5	130	2	C96820	hypothetical prote
113	7	1.7	1178	1	QVBYF	pyruvate carboxyla	186	6	1.5	131	2	S60913	hypothetical prote
114	7	1.7	1341	2	S09579	tail fiber protein	187	6	1.5	131	2	C75113	hypothetical prote
115	7	1.7	1388	2	T30335	KLP2 protein - Afr	188	6	1.5	132	2	A96600	protein F14J16.12
116	7	1.7	1568	2	T09074	semaphorin recepto	189	6	1.5	132	2	F64561	conserved hypothet
117	7	1.7	1667	2	T15863	protein F6N18.13 [190	6	1.5	133	2	T32385	hypothetical prote
118	7	1.7	1994	2	D86432	protein UNC-89 - C	191	6	1.5	136	2	D72245	ferric uptake regu
119	7	1.7	2957	2	T29757	hypothetical prote	192	6	1.5	137	1	ZXBPT4	uvay protein - pha
120	6	1.5	29	2	G90719	hypothetical prote	193	6	1.5	137	2	F83069	conductance mechan
121	6	1.5	29	2	T48910	KDPF protein [wall	194	6	1.5	137	2	AC2126	hypothetical prote
122	6	1.5	38	2	P90115	H-2 class I histoc	195	6	1.5	137	2	B75447	hypothetical prote
123	6	1.5	38	2	D4024	hypothetical prote	196	6	1.5	138	2	S69773	H+-transporting tw
124	6	1.5	48	2	S61469	p83/100 protein -	197	6	1.5	138	2	E71175	hypothetical prote
125	6	1.5	48	2	S61472	p83/100 protein -	198	6	1.5	138	2	C64237	hypothetical prote
126	6	1.5	53	2	T11383	Arpase subunit 8 -	199	6	1.5	138	2	D82400	TonB system transp
127	6	1.5	57	2	T03643	hypothetical prote	200	6	1.5	139	2	AI3059	hypothetical prote
128	6	1.5	60	2	A34138	6.8K proteolipid p	201	6	1.5	139	2	G98226	hypothetical prote
129	6	1.5	61	2	S13999	RNA-directed RNA p	202	6	1.5	140	2	S41785	dnaj protein - fis
130	6	1.5	62	2	B99006	hypothetical prote	203	6	1.5	142	2	JC5612	probable sugar tra
131	6	1.5	62	2	T51086	probable ubiquinol	204	6	1.5	142	2	JC5612	tropinin I beta -
132	6	1.5	64	2	B90340	hypothetical prote	205	6	1.5	142	2	S58082	transmembrane prot
133	6	1.5	66	2	F64395	hypothetical prote	206	6	1.5	142	2	JQ2280	low-temperature re
134	6	1.5	68	2	T10328	hypothetical prote	207	6	1.5	143	2	AH3060	hypothetical prote
135	6	1.5	70	2	S20770	Ig heavy chain V r	208	6	1.5	143	1	F46335	trans-regulatory s
136	6	1.5	78	2	S61468	p83/100 protein -	209	6	1.5	144	1	D97323	probable acetyltra
137	6	1.5	79	2	G64375	hypothetical prote	210	6	1.5	147	2	JQ2384	rev protein - feli
138	6	1.5	83	2	A36505	oxaloacetate decar	211	6	1.5	148	2	F75091	hypothetical prote
139	6	1.5	84	2	S61465	p83/100 protein -	212	6	1.5	148	2	B83120	hypothetical prote
140	6	1.5	84	2	S61466	p83/100 protein -	213	6	1.5	149	2	T08218	hypothetical prote
141	6	1.5	84	2	B81930	hypothetical prote	214	6	1.5	150	1	WMVZR2	17K protein - vacc
142	6	1.5	85	2	H45557	orf B downstream o	215	6	1.5	150	2	F72163	AIL protein - vari
143	6	1.5	89	2	T03072	probable zinc fing	216	6	1.5	150	2	C43517	AIL protein - vari
144	6	1.5	90	2	F82571	hypothetical prote	217	6	1.5	150	2	T28542	hypothetical prote
145	6	1.5	91	2	AE0547	probable secreted	218	6	1.5	150	2	T37387	superoxide dismuta
146	6	1.5	93	2	I48226	cryptdin-2 - mouse	219	6	1.5	152	2	JW0084	conserved hypothet
147	6	1.5	93	2	JF0055	baseplate protein	220	6	1.5	152	2	B70423	transcription regu
148	6	1.5	96	2	T31209	hypothetical prote	221	6	1.5	152	2	AD2512	hypothetical prote
149	6	1.5	98	2	E90606	hypothetical prote	222	6	1.5	152	2	B71608	probable coiled-co
150	6	1.5	102	2	T13512	hypothetical prote	223	6	1.5	153	2	E84218	hypothetical prote
151	6	1.5	102	2	T44994	probable tryptopha	224	6	1.5	154	2	S20511	superoxide dismuta
152	6	1.5	103	2	T39501	ribosomal protein	225	6	1.5	154	2	C81579	conserved hypothet
153	6	1.5	104	2	S74885	hypothetical prote	226	6	1.5	154	2	AD1065	sigma-54 dependent
154	6	1.5	105	2	C69068	divalent cation to	227	6	1.5	155	2	AD1553	hypothetical prote
155	6	1.5	107	2	S53575	probable membrane	228	6	1.5	155	2	T12815	hypothetical prote
156	6	1.5	107	2	F81747	hypothetical prote	229	6	1.5	156	2	A61017	phosphorylase hy
157	6	1.5	108	2	T52504	hypothetical prote	230	6	1.5	157	2	E71684	virg9 protein prec
158	6	1.5	110	2	G70618	probable pntAB pro	231	6	1.5	157	2	AC3462	hypothetical prote
159	6	1.5	110	2	B26848	hypothetical prote	232	6	1.5	158	2	B87730	protein Y2H5A.6 [
160	6	1.5	110	2	C95956	hypothetical prote	233	6	1.5	158	2	T69334	troponin C, skelet
161	6	1.5	112	2	T03411	ribosomal protein	234	6	1.5	159	1	TPPGCS	bacterioferritin I
162	6	1.5	112	2	A87239	pyridine transhydr	235	6	1.5	159	2	A87164	hypothetical prote
163	6	1.5	113	2	T15547	hypothetical prote	236	6	1.5	159	2	F83733	hypothetical prote
164	6	1.5	114	2	D70469	NADH2 dehydrogenas	237	6	1.5	159	2	B90363	hypothetical prote
165	6	1.5	116	2	T11541	alpha, 1-6-glucosi	238	6	1.5	160	1	T9PHCS	troponin C, fast s
166	6	1.5	116	2	T50029	alveolar macrophag	239	6	1.5	160	1	TPRBCS	troponin C, fast s
167	6	1.5	117	2	B42553	hypothetical prote	240	6	1.5	160	1	F69334	troponin C, skelet
168	6	1.5	117	2	A84151	hypothetical prote	241	6	1.5	161	2	T26727	conserved hypothet
169	6	1.5	118	2	H71564	type 4 fibrinase as	242	6	1.5	162	1	TPPGCS	hypothetical prote
170	6	1.5	118	2	D82777	hypothetical prote	243	6	1.5	162	2	F70324	hypothetical prote
171	6	1.5	118	2	E95881	hypothetical prote	244	6	1.5	162	2	AD1758	hypothetical prote
172	6	1.5	120	2	B71020	hypothetical prote	245	6	1.5	163	2	G84363	fast skeletal trop
173	6	1.5	120	2	F83244	hypothetical prote	246	6	1.5	163	2	JW0062	fast skeletal trop
174	6	1.5	122	1	Z12M49	22K zein (clone B4	247	6	1.5	163	2	JW0063	hypothetical prote
175	6	1.5	122	2	G90443	hypothetical prote	248	6	1.5	163	2	T10220	hypothetical prote

249	6	1.5	166	2	F90835	hypothetical prote	322	6	1.5	209	2	E85981	cell division prot
250	6	1.5	167	1	VKLJVS	trans-regulatory s	323	6	1.5	209	2	AH0425	ribosomal RNA larg
251	6	1.5	167	1	VKLJVA	trans-regulatory s	324	6	1.5	209	2	F84482	hypothetical prote
252	6	1.5	167	1	F45390	trans-regulatory s	325	6	1.5	210	2	A95045	DNA-binding respon
253	6	1.5	167	2	H98225	hypothetical prote	326	6	1.5	210	2	H97914	response regulator
254	6	1.5	167	2	T11897	metal stress-regul	327	6	1.5	210	2	T05298	hypothetical prote
255	6	1.5	168	1	S23323	Na+-transporting A	328	6	1.5	211	2	F75593	DNA-binding respon
256	6	1.5	168	2	T30923	hypothetical prote	329	6	1.5	211	2	T03355	gene el2 protein -
257	6	1.5	168	2	H85693	unknown protein en	330	6	1.5	211	2	AC3525	hypothetical prote
258	6	1.5	170	2	B82521	hypothetical prote	331	6	1.5	212	2	T13753	NADH2 dehydrogenas
259	6	1.5	170	2	G97106	uncharacterized co	332	6	1.5	212	2	S07552	coat protein - pea
260	6	1.5	171	2	D72090	hypothetical prote	333	6	1.5	213	2	H97177	response regulator
261	6	1.5	171	2	F86532	hypothetical prote	334	6	1.5	213	2	G88538	protein F58F6.7 [i
262	6	1.5	172	2	F69506	probable 2-oxoisov	335	6	1.5	214	2	JC5646	interleukin-1 beta
263	6	1.5	172	2	T04498	AIC2 protein homol	336	6	1.5	214	2	T09535	dnak-type molecula
264	6	1.5	173	2	S18035	pathogenesis-relat	337	6	1.5	217	2	S23536	hypothetical prote
265	6	1.5	173	2	S18034	pathogenesis-relat	338	6	1.5	218	2	B72116	hypothetical prote
266	6	1.5	173	2	A49624	polyprotein - chic	339	6	1.5	218	2	T22261	hypothetical prote
267	6	1.5	176	2	AB1930	phosphoribosylamin	340	6	1.5	219	2	S47082	dnak-type molecula
268	6	1.5	176	2	T29845	hypothetical prote	341	6	1.5	219	2	S47083	dnak-type molecula
269	6	1.5	177	2	T47133	hypothetical prote	342	6	1.5	220	1	RWU28	T-cell surface gly
270	6	1.5	179	2	C65006	hypothetical prote	343	6	1.5	220	2	T51648	probable transcrip
271	6	1.5	179	2	F72652	hypothetical prote	344	6	1.5	220	2	AE2360	hypothetical prote
272	6	1.5	179	2	B82143	conserved hypothet	345	6	1.5	221	2	S24327	glutathione peroxi
273	6	1.5	179	2	S75860	hypothetical prote	346	6	1.5	221	2	S39878	carr protein - Myx
274	6	1.5	180	2	H64542	hypothetical prote	347	6	1.5	221	2	T15784	hypothetical prote
275	6	1.5	180	2	H71965	hypothetical prote	348	6	1.5	221	2	D84780	hypothetical prote
276	6	1.5	180	2	D90569	hypothetical prote	349	6	1.5	222	2	E71652	hypothetical prote
277	6	1.5	180	2	T47031	hypothetical prote	350	6	1.5	223	2	T44784	regulatory protein
278	6	1.5	180	2	AB0235	probable transcrip	351	6	1.5	223	2	B81378	two-component regu
279	6	1.5	181	2	AG1368	NADH-dependent FMN	352	6	1.5	223	2	S34018	hypothetical prote
280	6	1.5	182	2	D82490	hypothetical prote	353	6	1.5	223	2	A64633	phosphotransacetyl
281	6	1.5	183	2	C64363	TATA-binding trans	354	6	1.5	223	2	B83943	hypothetical prote
282	6	1.5	183	2	D90335	terminal quinol ox	355	6	1.5	224	2	D64454	proteasome beta su
283	6	1.5	183	2	T25711	hypothetical prote	356	6	1.5	224	2	E95223	hypothetical prote
284	6	1.5	184	2	T51655	myb-related transc	357	6	1.5	224	2	T34686	probable integral
285	6	1.5	184	2	AD1127	hypothetical prote	358	6	1.5	224	2	H98087	hypothetical prote
286	6	1.5	185	1	A47196	dual specificity p	359	6	1.5	226	1	NRE3	RNase III (importe
287	6	1.5	185	2	G82609	conserved hypothet	360	6	1.5	226	2	A91058	RNase III, ds RNA
288	6	1.5	186	2	B69832	biotin biosynthesi	361	6	1.5	226	2	F85302	ribonuclease III (
289	6	1.5	186	2	S46093	probable membrane	362	6	1.5	226	2	AC0829	ATP synthase F0 ch
290	6	1.5	188	2	S73096	hypothetical prote	363	6	1.5	227	2	F90614	photosystem I chai
291	6	1.5	189	2	S49581	apolipoprotein D -	364	6	1.5	227	2	S04133	response regulator
292	6	1.5	190	2	T37707	hypothetical prote	365	6	1.5	228	2	D96964	probable translati
293	6	1.5	191	2	C40364	hypothetical prote	366	6	1.5	228	2	H72703	probable haloacid
294	6	1.5	192	2	JH0171	visinin - chicken	367	6	1.5	229	2	E75005	aquaporin Z PA4034
295	6	1.5	192	2	C70487	transcription regu	368	6	1.5	229	2	F83141	hypothetical prote
296	6	1.5	193	2	H91249	hypothetical prote	369	6	1.5	229	2	H75205	probable DNA repai
297	6	1.5	194	2	T17381	vrl8 protein - Dic	370	6	1.5	230	2	A96836	hypothetical prote
298	6	1.5	196	2	QJ1078	stylak glycoprotei	371	6	1.5	230	2	A75260	probable haloacid
299	6	1.5	196	2	AI1361	probable scaffold	372	6	1.5	232	2	D71157	DNA repair protein
300	6	1.5	196	2	AC2307	hypothetical prote	373	6	1.5	232	2	H84028	hypothetical expor
301	6	1.5	197	2	B83768	hypothetical prote	374	6	1.5	232	2	AF3406	probable membrane
302	6	1.5	199	2	S50363	nitrilase homolog	375	6	1.5	233	2	AB0273	hypothetical prote
303	6	1.5	200	2	AC0343	probable CDP-alcoh	376	6	1.5	233	2	T25295	hypothetical prote
304	6	1.5	200	2	H85042	hypothetical prote	377	6	1.5	235	2	T22826	probable TetR-fami
305	6	1.5	200	2	D75059	hypothetical prote	378	6	1.5	236	2	C87244	nodulin 21-related
306	6	1.5	200	2	B97001	transcription regu	379	6	1.5	236	2	F75375	hypothetical membr
307	6	1.5	201	1	Q6BE18	UL92 protein - hum	380	6	1.5	237	2	D95938	ribosomal protein
308	6	1.5	201	2	S62757	NADH2 dehydrogenas	381	6	1.5	238	2	F71723	probable membrane
309	6	1.5	201	2	T44594	alcaligin syntheti	382	6	1.5	238	2	T35088	hypothetical prote
310	6	1.5	202	2	G85439	cold acclimation p	383	6	1.5	239	2	F75111	coat protein - nar
311	6	1.5	205	2	B95285	conserved hypothet	384	6	1.5	240	1	VCWGN4	hypothetical prote
312	6	1.5	205	2	A85506	GMP kinase [import	385	6	1.5	241	2	AB1998	hypothetical prote
313	6	1.5	205	2	F72117	guanylate kinase C	386	6	1.5	242	2	AB3252	arabinose phosphat
314	6	1.5	206	2	S38626	glutathione transp	387	6	1.5	242	2	B81397	pyridoxal phosphate
315	6	1.5	206	2	A55412	lymphocyte phospho	388	6	1.5	242	2	H81833	pyridoxal phosphate
316	6	1.5	208	1	GXBPT4	baseplate protein	389	6	1.5	242	2	AB6189	protein T25N20.7 [
317	6	1.5	208	2	AH0902	cell division prot	390	6	1.5	243	2	C72776	hypothetical prote
318	6	1.5	208	2	T34512	hypothetical prote	391	6	1.5	244	2	A87633	hydroxylase, alpha/b
319	6	1.5	208	2	T51775	3-hydroxybutyryl-C	392	6	1.5	244	2	JN0487	acetate decar
320	6	1.5	209	2	S35108	23S rRNA methyltra	393	6	1.5	244	2	B71022	hypothetical prote
321	6	1.5	209	2	B91136	cell division prot	394	6	1.5	245	2	D87612	3'-deoxy-manno-octu

395 245 2 B70480 ribosomal protein
396 247 2 C71722 hypothetical prote
397 249 2 G97110 ATPase component c
398 250 2 F72247 methionine aminope
399 251 2 D69470 conserved hypoteth
400 251 2 G72118 conserved hypoteth
401 251 2 H86504 C7021 hypothetical
402 251 2 T22839 hypothetical prote
403 253 2 G89850 triosephosphate is
404 253 2 A55183 GS2 protein - huma
405 255 2 S26030 cytochrome-c oxida
406 255 2 S26032 cytochrome-c oxida
407 255 2 S53099 nes protein - huma
408 256 2 T11233 Hs-transporing tw
409 256 2 T11233 PMS3 homolog mma
410 257 2 C98027 hypothetical prote
411 258 2 A43692 T1 protein - rabbi
412 258 2 G84824 hypothetical prote
413 259 2 T12386 NADH2 dehydrogenas
414 259 2 C81008 methionine aminope
415 259 2 E82029 methionyl aminopep
416 259 2 A70359 hydroxylase expres
417 259 2 C70708 hypothetical prote
418 259 2 A69476 conserved hypoteth
419 260 2 T12388 NADH2 dehydrogenas
420 260 2 T12394 NADH2 dehydrogenas
421 260 2 T12395 NADH2 dehydrogenas
422 260 2 T01145 probable acetone-c
423 261 2 S47724 hypothetical 29.5K
424 261 2 S21935 probable MAS-box
425 261 2 T09603 MADS-box protein 3
426 261 2 A70676 hypothetical prote
427 261 2 D95193 ylmH protein [impo
428 261 2 T46138 myb-like protein -
429 261 2 B96358 F12K8.16 protein -
430 262 2 A82956 probable beta-lact
431 264 2 A21233 ATP-binding protei
432 264 2 H64086 glycerol facilitat
433 264 2 E95119 hypothetical prote
434 264 2 B97989 hypothetical prote
435 265 2 S64938 hypothetical prote
436 266 2 C84365 electron transfer
437 266 2 A81223 glutamate racemase
438 267 2 G83760 pyrroline-5-carbox
439 267 2 S09672 kafirin precursor
440 267 2 T33911 hypothetical prote
441 268 2 S71200 agamous-like prote
442 268 2 I52726 microtubule-associ
443 269 2 S04124 kafirin precursor
444 269 2 T36001 probable integral
445 270 2 S20520 chlorophyll a/b-bi
446 270 2 G96686 hypothetical prote
447 271 2 G89929 hypothetical prote
448 271 2 B84861 50S ribosomal prot
449 273 2 A86280 F14117.29 protein
450 274 2 A43719 ureD protein - Pro
451 275 2 H71690 hypothetical prote
452 276 2 T12552 hypothetical prote
453 276 2 A71653 hypothetical prote
454 276 2 B96996 hypothetical prote
455 276 2 B82443 hypothetical prote
456 277 2 B75007 probable translati
457 277 2 G97783 hypothetical prote
458 278 2 C43670 integral membrane
459 278 2 A47090 urase-associated
460 279 2 D69003 biopolymer transpo
461 281 2 H64125 modb protein homol
462 281 2 T22291 hypothetical prote
463 282 2 E70440 deoxyribonuclease
464 282 2 T07303 cell division inhi
465 282 2 T35000 probable protein a
466 283 2 S25610 dihydropterate sy
467 283 2 A99060 conserved hypoteth

468 6 1.5 284 2 A55455 steroidogenic acut
469 6 1.5 284 2 S60250 mab-18 protein (tr
470 6 1.5 284 2 E83557 probable transcrip
471 6 1.5 284 2 ACO331 probable membrane
472 6 1.5 285 2 B71194 probable integrase
473 6 1.5 285 2 S76841 hypothetical prote
474 6 1.5 285 2 A84494 envelope-like prot
475 6 1.5 286 2 F69801 epoxide hydrolase
476 6 1.5 286 2 S76741 sulfate transport
477 6 1.5 286 2 A75153 integrase/recombin
478 6 1.5 286 2 E69516 hypothetical prote
479 6 1.5 287 2 T22324 hypothetical prote
480 6 1.5 289 2 A81846 sulfate transport
481 6 1.5 289 2 B89991 truncated beta-hem
482 6 1.5 289 2 S64254 hypothetical prote
483 6 1.5 290 2 A84011 transcription acti
484 6 1.5 290 2 H64374 type II restrictio
485 6 1.5 291 2 F97198 oxygen-independent
486 6 1.5 292 2 T30267 sugar transport pr
487 6 1.5 292 2 F71901 hypothetical prote
488 6 1.5 292 2 E64614 beta-alanine synth
489 6 1.5 292 2 S77139 hypothetical prote
490 6 1.5 292 2 S73692 probable GTPase/GT
491 6 1.5 294 2 G69356 L-malate dehydroge
492 6 1.5 294 2 G83962 hypothetical prote
493 6 1.5 294 2 B83964 hypothetical prote
494 6 1.5 295 2 S52791 aryl sulfotransfer
495 6 1.5 295 2 JCS249 aryl sulfotransfer
496 6 1.5 295 2 G01843 aryl sulfotransfer
497 6 1.5 295 2 S34544 hypothetical prote
498 6 1.5 295 2 T22039 hypothetical prote
499 6 1.5 295 2 T23379 hypothetical prote
500 6 1.5 296 2 H83988 transcription regu

ALIGNMENTS

RESULT 1

A69484
hypothetical protein AF1874 - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Nov-2000

C/Accession: A69484

R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Burton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A/Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S

Smith, H.O.; Woese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A/Reference number: A69250; MUID:98049343; PMID:9389475

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-546 <KLE>

A/Cross-references: GB:AE000782; GB:AE000973; GB:AE000782; NID:G2689296; PIDN:AB89382.1; PID:G26486

C/Superfamily: Pyrococcus horikoshii probable helicase PH0917

Query Match 2.2%; Score 9; DB 2; Length 546;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 221 SLQELKSI 229

Db 62 SLQELKSI 70

RESULT 2

A13522

tauxine transport system permease protein tauC [imported] - Brucella melitensis (strain

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-feb-2002 #text_change 15-Feb-2002

C/Accession: A13522
 R;DelVecchio, V.G.; Kapatal, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A/Title: The genome sequence of the facultative intracellular pathogen *Bruceella melitensis*
 A/Reference number: AD3252; PMID:11756688
 A/Accession: A13522
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-246 <KUR>
 A/Cross-references: GB:AE008918; PIDN:AA153348.1; PID:gl7984237; GSPDB:GN00191
 A/Experimental source: strain 16M
 C/Genetics:
 A/Map position: II
 C/Superfamily: *Synechococcus* nitrate transport protein nrtB

Query Match 2.0%; Score 8; DB 2; Length 246;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VLSGFVLG 16
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 DB 63 VLSGFVLG 70

RESULT 3
 P97610
 Hypothetical protein CC2920 [imported] - *Caulobacter crescentus*
 C/Species: *Caulobacter crescentus*
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C/Accession: F87610
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A/Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A/Reference number: AB7249; MUID:21173698; PMID:11259647
 A/Accession: F87610
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-297 <STC>
 A/Cross-references: GB:AE005673; NID:gl3424542; PIDN:AAK24882.1; GSPDB:GN00148
 C/Genetics:
 A/Gene: CC2920

Query Match 2.0%; Score 8; DB 2; Length 297;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LLGEVKGE 40
 |||||
 DB 267 LLGEVKGE 274

RESULT 4
 T40912
 Probable lectin precursor - fission yeast (*Schizosaccharomyces pombe*)
 C/Species: *Schizosaccharomyces pombe*
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T40912
 R;Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, December 1998
 A/Reference number: Z21956
 A/Accession: T40912
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-312 <MUR>
 A/Cross-references: EMBL:AL034490; PIDN:CAA22477.1; GSPDB:GN00068; SPDB:SPCC126.08C
 A/Experimental source: strain 972h-; cosmid c126
 C/Genetics:
 A/Gene: SPDB:SPCC126.08C
 A/Map position: 3

Query Match 2.0%; Score 8; DB 2; Length 312;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFVLGALA 19
 |||||
 DB 15 GFVLGALA 22

RESULT 5
 AG2924
 tRNA modification GTPase [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
 C/Species: *Agrobacterium tumefaciens*
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C/Accession: AG2924
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A/Reference number: AB2577; MUID:21608550; PMID:11743193
 A/Accession: AG2924
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-442 <KUR>
 A/Cross-references: GB:AE008698; PIDN:AA143813.1; PID:gl7741353; GSPDB:GN00186
 A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A/Gene: thdF
 A/Map position: circular chromosome
 C/Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu hom

Query Match 2.0%; Score 8; DB 2; Length 442;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEKR 257
 |||||
 DB 361 LKREIEKR 368

RESULT 6
 F97698
 Probable thiophen and furan oxidation protein thdF [imported] - *Agrobacterium tumefaci*
 C/Species: *Agrobacterium tumefaciens*
 C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C/Accession: F97698
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.
 Science 294, 2323-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tu*
 A/Reference number: A97359; MUID:21608551; PMID:11743194
 A/Accession: F97698
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-442 <KUR>
 A/Cross-references: GB:AE007869; PIDN:AAK88543.1; PID:gl5158062; GSPDB:GN00169
 C/Genetics:
 A/Gene: AGR C 5135
 A/Map position: circular chromosome
 C/Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu hom

Query Match 2.0%; Score 8; DB 2; Length 442;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEKR 257
 |||||
 DB 361 LKREIEKR 368

RESULT 7
T49272
hypothetical protein T21J18.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49272
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25021
A;Accession: T49272
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <RI>
A;Cross-references: ENBL:ALJ32963; GSPDB:GN00061; ATSP:T21J18.30
A;Experimental source: cultivar Columbia; BAC clone T21J18
C;Genetics:
A;Gene: ATSP:T21J18.30
A;Map position: 3
A;introns: 37/3; 92/3; 191/3; 269/3

Query Match 2.0%; Score 8; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLLT 136
|||
Db 93 DLVFLLLT 100

RESULT 8
T43738
dnaK-type molecular chaperone dnaK [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
R;Hanawa, T.; Kai, M.; Kamiya, S.; Yamamoto, T.
submitted to the EMBL Data Library, February 1999
A;Description: Cloning, sequencing, and transcriptional analysis of the dnaK heat shock
A;Reference number: Z22656
A;Accession: T43738
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-613 <HAN>
A;Cross-references: ENBL:AB023064; PIDN:BAA82789.1
A;Experimental source: strain 10403S
C;Genetics:
A;Note: dnaK
C;Superfamily: heat shock protein 70
C;Keywords: molecular chaperone; stress-induced protein

Query Match 2.0%; Score 8; DB 2; Length 613;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 397
|||
Db 478 TDEIEK 485

RESULT 9
AE1621
class I heat-shock protein (molecular chaperone) DnaK [imported] - Listeria innocua (str
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AE1621
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1621
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-613 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96741.1; PID:G16413983; GSPDB:GN00178
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: dnaK
C;Superfamily: heat shock protein 70

Query Match 2.0%; Score 8; DB 2; Length 613;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 397
|||
Db 478 TDEIEK 485

RESULT 10
AI1258
class I heat-shock protein (molecular chaperone) DnaK [imported] - Listeria monocytogen
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AI1258
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AI1258
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-613 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99551.1; PID:G16410902; GSPDB:GN00177
A;Experimental source: strain EGB-e
C;Genetics:
A;Gene: dnaK
C;Superfamily: heat shock protein 70

Query Match 2.0%; Score 8; DB 2; Length 613;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 397
|||
Db 478 TDEIEK 485

RESULT 11
I51617
kinesin-like protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Feb-2001
C;Accession: I51617; A48835; S48837
R;Vernos, I.; Raats, J.; Hirano, T.; Heasman, J.; Karsenti, E.; Wylie, C.
Cell 81, 117-127, 1995
A;Title: Xklp1, a chromosomal Xenopus kinesin-like protein essential for spindle organi
A;Reference number: A56221; MUID:95236444; PMID:7720067
A;Accession: I51617
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1226 <VER>
A;Cross-references: EMBL:X82012; NID:G562792; PIDN:CAA57539.1; PID:G562793
Dev. Biol. 157, 232-239, 1993
R;Vernos, I.; Heasman, J.; Wylie, C.
A;Title: Multiple kinesin-like transcripts in Xenopus oocytes.
A;Reference number: A48835; MUID:93246065; PMID:8482413
A;Accession: A48835

A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 9-162, 'L', 164-338 <VE2>
 A:Experimental source: oocyte
 A>Note: sequence extracted from NCBI backbone (NCBIP:130975)
 C:Genetics:
 A:Gene: klpi

C:Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology
 C:Keywords: ATP; nucleotide binding; P-loop
 F:9-343/Domain: kinesin motor domain homology <KXOT>
 F:87-94/Region: nucleotide-binding motif A (P-loop)

Query Match 2.0%; Score 8; DB 2; Length 1226;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 391 DEEIEKMK 398
 |||||
 Db 974 DEEIEKMK 981

RESULT 12

D83736 hypothetical protein BH0692 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: D83736
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: D83736
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-92 <STO>
 A:Cross-references: GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA04411.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH0692

Query Match 1.7%; Score 7; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 ERLHKN 120
 |||||
 Db 16 ERLHKN 22

RESULT 13

S00120 hypothetical protein D - proteus vulgaris

C:Species: Proteus vulgaris
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 29-Sep-1999
 C:Accession: S00120
 R:Coile, S.T.
 Eur. J. Biochem. 167, 481-488, 1987

A>Title: Nucleotide sequence and comparative analysis of the frd operon encoding the fun
 d-linked ampC cephalosporinase gene.

A:Reference number: S00107; MUID:88004470; PMID:3308458

A:Accession: S00120

A:Molecule type: DNA

A:Residues: 1-104 <COL>

A:Cross-references: EMBL:X06151; NID:G45907; PIDN:CAA29512.1; PID:G45911

C:Superfamily: sugE protein

C:Keywords: transmembrane protein

F:2-20/Domain: transmembrane #status predicted <TM1>

F:29-48/Domain: transmembrane #status predicted <TM2>

F:57-78/Domain: transmembrane #status predicted <TM3>

Query Match 1.7%; Score 7; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 LTPSIIT 141
 |||||
 Db 29 LTPSIIT 35

RESULT 14

AC0044

probable chaperone sugE [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C:Accession: AC0044

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001

A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AC0044

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89214.1; PID:gl5978453; GSPDB:GN00175

C:Genetics:

A:Gene: sugE

C:Superfamily: sugE protein

Query Match 1.7%; Score 7; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 LTPSIIT 141
 |||||
 Db 29 LTPSIIT 35

RESULT 15

AE1046

SugE protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT1
 C:Species: Salmonella enterica subsp. enterica serovar Typhi

A>Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AE1046

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
 th, T.; Conner, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AE1046

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD06818.1; PID:gl6505469; GSPDB:GN00176

C:Genetics:

A:Gene: sugE

C:Superfamily: sugE protein

Query Match 1.7%; Score 7; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 LTPSIIT 141
 |||||
 Db 29 LTPSIIT 35

RESULT 16

B75086

hypothetical protein BAB0720 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C;Accession: B75086
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: B75086
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KAW>
A;Cross-references: GB:AJ248286; GB:AL096836; NID:G5458366; PIDN:CAB49991.1; PID:sl51588
A;Experimental source: strain Orey
C;Genetics:
A;Gene: PAB0720

Query Match 1.7%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIEKMK 398
|||||
Db 98 EEIEKMK 104

RESULT 17
AE1379
hypothetical protein lmc2437 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE1379
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AE1077; MUID:21537279; PMID:11679669
A;Accession: AE1379
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <GLA>
A;Cross-references: GB:NC 003210; PIDN:CAD00515.1; PID:gl6411925; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmc2437

Query Match 1.7%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 QAVDKLV 244
|||||
Db 86 QAVDKLV 92

RESULT 18
T26693
hypothetical protein Y38H6C.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26693
R;White, S.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z20255
A;Accession: T26693
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-140 <WIL>
A;Cross-references: EMBL:AL031630; PIDN:CAA20983.1; GSPDB:GN00023; CESP:Y38H6C.3
A;Experimental source: clone Y38H6C
C;Genetics:
A;Gene: CESP:Y38H6C.3
A;Map position: 5

A;Introns: 22/3; 61/3; 111/2

Query Match 1.7%; Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 REIEKRR 258
|||||
Db 44 REIEKRR 50

RESULT 19
AE2617
nitrogen regulatory IIA protein ptsN [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AB2617
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.; erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McGlellan, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2617
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-153 <KUR>
A;Cross-references: GB:AB008688; PIDN:AAL41352.1; PID:gl17738666; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: ptsN
A;Map position: circular chromosome
C;Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-1-

Query Match 1.7%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
|||||
Db 97 DLVFLLL 103

RESULT 20
B97399
nitrogen regulatory IIA protein (enzyme IIA-ntx) (phosphotransferase enzyme II, a compo
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: B97399
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97399
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-153 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86147.1; PID:gl5155236; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_576
A;Map position: circular chromosome
C;Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-1-

Query Match 1.7%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
|||||
Db 97 DLVFLLL 103

RESULT 21

AD3475
protein-Npi-phosphohistidine-sugar phosphotransferase (EC 2.7.1.69) [imported] - Brucella
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C/Accession: AD3475
R/Delvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Parra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesh
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A/Reference number: AD3252; PMID:11756688
A/Accession: AD3475
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-154 <KUN>
A/Cross-references: GB:AB008917; PIDN:AAU52967.1; PID:gl7983918; GSPDB:GN00150
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BMEI1786
A/Map position: 1
C/Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-
C/Keywords: phosphotransferase

Query Match 1.7%; Score 7; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLL 135

DB 97 DLVFLL 103

RESULT 22

H70004
conserved hypothetical protein ytzF - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C/Accession: H70004
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Enian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Kotter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: AG9580; PMID:98044033; PMID:9384377
A/Accession: H70004
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-157 <KUN>
A/Cross-references: GB:Z99119; GB:ALC09126; NID:G2635411; PIDN:CAB14981.1; PID:G2635487
A/Experimental source: strain 168
C/Genetics:
A/Gene: ytzF
C/Superfamily: Mycobacterium tuberculosis hypothetical protein RV1711

Query Match 1.7%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 DTEGFL 34

DB 23 DTEGFL 29

RESULT 23

S64213
hypothetical protein YGL196w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein G1315
C/Species: Saccharomyces cerevisiae
C/Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C/Accession: S64213; S62049
R/Brusch, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64183
A/Accession: S64213
A/Molecule type: DNA
A/Residues: 1-165 <BRU>
A/Cross-references: EMBL:Z72718; NID:gl322822; PIDN:CAA96908.1; PID:gl322823; MIPS:YGL1.
A/Experimental source: strain S288C
R/Klima, R.; Coglievina, M.; Bertani, I.; Zaccaria, P.; Brusch, C.V.
submitted to the EMBL Data Library, September 1995
A/Reference number: S62045
A/Accession: S62049
A/Molecule type: DNA
A/Residues: 1-147, RTRDTEANKLERVNS;TKLSKIAVLPHQACITMGQPPYFVNVNSEIGVNDVLPFOKW' <KLI>
A/Cross-references: EMBL:X91837; NID:gl177627; PIDN:CAA62948.1; PID:gl177632
A/Experimental source: strain FY1679
C/Genetics:
A/Cross-references: SGD:S0003164
A/Map position: 7L
C/Superfamily: Saccharomyces cerevisiae hypothetical protein YGL196w

Query Match 1.7%; Score 7; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LSGFVLG 16

DB 84 LSGFVLG 90

RESULT 24

E90621
NADH dehydrogenase chain 6 ND6 [imported] - Tinamus major mitochondrion
C/Species: mitochondrion Tinamus major
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 03-Aug-2001
C/Accession: E90621
R/Hadgraft, O.; Baker, A.J.
Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001
A/Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogen
A/Reference number: A99613; MUID:21263106; PMID:11370967
A/Accession: E90621
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-173 <KUR>
A/Cross-references: GB:NC_002781; NID:gl4141960; PIDN:NP_115401.1; GSPDB:GN00160
C/Genetics:
A/Gene: ND6
A/Genome: mitochondrion
A/Genetic code: SGC1
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 6
C/Keywords: mitochondrion

Query Match 1.7%; Score 7; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19

DB 12 FVLGALA 18

RESULT 25

E90617
NADH dehydrogenase chain 6 ND6 [imported] - Pterocnemia pennata mitochondrion

C:Species: mitochondrion Pterocnemis pennata
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 03-Aug-2001
 A:Accession: E30617
 R:Hadrath, O.; Baker, A.J.
 Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001
 A:Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogeny
 A:Reference number: A99613; MUID:21263106; PMID:11370967
 A:Accession: E30617
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-174 <KUR>
 A:Cross-references: GB:NC_002783; NID:G14141904; PIDN:NP_115427.1; GSPDB:GN00158
 C:Genetics:
 A:Gene: ND6
 A:Genome: mitochondrion
 A:Genetic code: SGC1
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 6
 C:Keywords: mitochondrion

Query Match 1.7%; Score 7; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
 |||||
 Db 13 FVLGALA 19

RESULT 26
 T37444
 Probable 20.7K protein - vaccinia virus (strain Ankara)
 C:Species: vaccinia virus
 A:Variety: strain Ankara
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 15-Sep-2003
 A:Accession: T37444
 R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
 submitted to the EMBL Data Library, March 1997
 A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
 A:Reference number: Z30877
 A:Accession: T37444
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-177 <ANT>
 A:Cross-references: EMBL:U94848; PIDN:AAB96549.1
 A:Experimental source: strain Ankara
 C:Genetics:
 A:Note: MVA175R
 C:Superfamily: uncharacterized conserved protein

Query Match 1.7%; Score 7; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
 |||||
 Db 62 SIITESC 68

RESULT 27
 JQ1801
 B7R 21.3K protein precursor - vaccinia virus (strains WR and Copenhagen)
 C:Species: vaccinia virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
 A:Accession: JQ1801; E38550; F42526
 R:Smith, G.L.; Chan, Y.S.; Howard, S.T.
 J. Gen. Virol. 72, 1349-1376, 1991
 A:Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right in
 A:Reference number: JQ1767; MUID:91259063; PMID:2045793
 A:Accession: JQ1801
 A:Molecule type: DNA
 A:Residues: 1-182 <SMI>
 A:Cross-references: DDBJ:D11079; NID:G222717; PIDN:BA01837.1; PID:G222752; GB:M58056; N
 T09390
 A:Experimental source: strain WR

R:Howard, S.T.; Chan, Y.S.; Smith, G.L.
 Virology 180, 633-647, 1991
 A:Title: Vaccinia virus homologues of the Shope fibroma virus inverted terminal repeat
 A:Reference number: A38550; MUID:91111982; PMID:1846491
 A:Accession: E38550
 A:Molecule type: DNA
 A:Residues: 1-182 <HOW>
 A:Cross-references: GB:M58052
 R:Johnson, G.P.
 submitted to GenBank, June 1990
 A:Reference number: A33172
 A:Accession: F42526
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-182 <JOH>
 A:Experimental source: strain Copenhagen
 C:Superfamily: uncharacterized conserved protein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-182/Product: B7R protein #status predicted <MAI>

Query Match 1.7%; Score 7; DB 2; Length 182;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 SIITESC 144
 |||||
 Db 62 SIITESC 68

RESULT 28
 T00519
 Proline-rich protein At2g23130 - Arabidopsis thaliana
 N:Alternate names: protein T20D16.24
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 A:Accession: T00519; H84620
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
 submitted to the EMBL Data Library, November 1997
 A:Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
 A:Reference number: Z14164
 A:Accession: T00519
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-185 <ROU>
 A:Cross-references: EMBL:AC002391; NID:G2642427; PID:G2642449
 A:Experimental source: Cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Niezman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.W.; Venter,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: H84620
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-185 <STO>
 A:Cross-references: GB:AE002093; NID:G2642449; PIDN:AAB87117.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: T20D16.24; At2g23130
 A:Map position: 2
 A:Introns: 158/3

Query Match 1.7%; Score 7; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 PASTPQI 343
 |||||
 Db 76 PASTPQI 82

RESULT 29
 T09390

21K protein precursor - alfalfa
 C:Species: Medicago sativa (alfalfa)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: T09390
 R:Coronado, C.
 submitted to the EMBL Data Library, February 1997
 A:Reference number: Z16658
 A:Accession: T09390
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-187 <OR>
 A:Cross-references: EMBL:Y11553; NID:e1029850; PID:g304664
 A:Species: Bacillus halodurans
 A:Experimental source: strain A2, subspecies varia; nodule
 F1-18/Domain: signal sequence #status predicted <SG>
 F19-187/Product: 21 K protein #status predicted <Mar>

Query Match 1.7%; Score 7; DB 2; Length 187;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFLLLT 136
 DB 7 LVFLLLT 13

RESULT 30
 G84018
 Hypothetical protein BH2951 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: G84018
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: G84018
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-190 <STO>
 A:Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA806670.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH2951

Query Match 1.7%; Score 7; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 PLVWNL 171
 DB 95 PLVWNL 101

RESULT 31
 T18495
 Hypothetical protein C0795w - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C:Accession: T18495
 R:Lawson, D.; Bowman, S.; Barrell, B.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z18935
 A:Accession: T18495
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-202 <LAW>
 A:Cross-references: EMBL:Z98551; NID:e1331903; PID:e1331916; PIDN:CAB11134.1
 C:Genetics:
 A:Map position: 3
 A:Note: C0795w

Query Match 1.7%; Score 7; DB 2; Length 202;
 Best Local Similarity 100.0%; Pred. No. 60;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LKKILSN 91
 DB 112 LKKILSN 118

RESULT 32
 B64357
 Hypothetical protein homolog MJ0458 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Aug-2003
 C:Accession: B64357
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
 A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: B64357
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-216 <BUL>
 A:Cross-references: GB:U67496; GB:L77117; NID:g2826283; PIDN:AA898446.1; PID:g1499252;
 C:Genetics:
 A:Map position: FOR409196-409846
 C:Superfamily: kinase with amino acid kinase domain

Query Match 1.7%; Score 7; DB 1; Length 216;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
 DB 89 LKREIEK 95

RESULT 33
 T22259
 Hypothetical protein F46A8.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T22259
 R:Harris, B.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19539
 A:Accession: T22259
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-228 <WIL>
 A:Cross-references: EMBL:Z81539; PIDN:CAB04389.1; GSPDB:GN00019; CESP:F46A8.3
 A:Experimental source: clone F46A8
 C:Genetics:
 A:Gene: CESP:F46A8.3
 A:Map position: 1
 A:Introns: 149/3

Query Match 1.7%; Score 7; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFLLLT 136
 DB 3 LVFLLLT 9

RESULT 34
 H84119
 ATP synthase subunit a atpB [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: H84119

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84119
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <STO>
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA07479.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: atpB
C;Superfamily: H⁺-transporting ATP synthase protein 6

Query Match 1.7%; Score 7; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 397 MKGFGGY 403
DB 135 MKGFGGY 141

RESULT 35
H97081
proline/glycine betaine ABC transport system, ATPase component CAC1475 [imported] - Clostr
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: H97081
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97081
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79443.1; PID:g15024420; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1475

Query Match 1.7%; Score 7; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 251 KREIEKR 257
DB 111 KREIEKR 117

RESULT 36
B69197
conserved hypothetical protein MTH727 - Methanobacterium thermoautotrophicum (strain Del
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 06-Jan-2003
C;Accession: B69197
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69197
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-256 <MTH>
A;Cross-references: GB:AE000852; GB:AE000666; NID:g2621812; PIDN:AA858232.1; PID:g262181
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH727
A;Start codon: TTG

C;Superfamily: uncharacterized conserved protein

Query Match 1.7%; Score 7; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 LSGFVLG 16
DB 39 LSGFVLG 45

RESULT 37
D95161
hypothetical protein SP1387 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: D95161
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
A;Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: D95161
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75485.1; PID:g14972874; GSPDB:GN00164; TIGR:SP
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1387
C;Superfamily: spermidine/putrescine transport system permease protein potI

Query Match 1.7%; Score 7; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 135 LTPSIIT 141
DB 179 LTPSIIT 185

RESULT 38
AF0024
peptidylprolyl isomerase (EC 5.2.1.8) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 01-Feb-2002
C;Accession: AF0024
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0024
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89056.1; PID:g15978296; GSPDB:GN00175
C;Genetics:
A;Gene: fkpA
C;Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl
C;Keywords: cis-trans-isomerase

Query Match 1.7%; Score 7; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 390 TDEIEIK 396
DB 91 TDEIEIK 97

```
RESULT 39
H95122
ABC-2 transporter, permease protein, probable SPI063 [imported] - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: H95122
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
non, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95122
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75177.1; PID:g14972538; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI063

Query Match      1.7%; Score 7; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 LVFLLLT 136
    |||||
Db 238 LVFLLLT 244

RESULT 40
D64456
protein-export membrane protein - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: D64456
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
ison, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: D64456
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-282 <BUL>
A:Cross-references: GB:U67565; GB:L77117; NID:g1591874; PIDN:AAB99256.1; PID:g1591886; T
C:Genetics:
A:Map position: REV1195831-1194983
C:Superfamily: Methanobacterium thermoautotrophicum protein-export membrane protein secP

Query Match      1.7%; Score 7; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 SSKFFEE 205
    |||||
Db 114 SSKFFEE 120

RESULT 41
T51837
MTN3 homolog [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana [mouse-ear cross]
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51837
R:Cheong, J.J.
submitted to the EMBL Data Library, September 1998
A:Description: An Arabidopsis cDNA clone encoding a protein homologous to Medicago trunc
A:Reference number: Z25480
```

```
A:Accession: T51837
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-285 <CHE>
A:Cross-references: EMBL:AF095641; PIDN:AA64192.1
C:Genetics:
A:Note: MTN3

Query Match      1.7%; Score 7; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GFVLGAL 18
    |||||
Db 200 GFVLGAL 206

RESULT 42
A37818
osteopontin precursor - mouse
N:Alternate names: Bone sialoprotein I; early T lymphocyte activation 1 protein; phosph
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 27-Jun-1994 #text_change 10-Sep-1999
A:Accession: A37818; S04078; S12064; A33853; J0105; A60931; S11677
R:Miyazaki, Y.; Setoguchi, M.; Yoshida, S.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.
J. Biol. Chem. 265, 14432-14438, 1990
A:Title: The mouse osteopontin gene. Expression in monocytic lineages and complete nucl
A:Reference number: A37818; MUID:90354433; PMID:2387863
A:Accession: A37818
A:Molecule type: DNA
A:Residues: 1-294 <MIY>
A:Cross-references: EMBL:X51834
R:Miyazaki, Y.; Setoguchi, M.; Yoshida, S.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.
Nucleic Acids Res. 17, 3298, 1989
A:Title: Nucleotide sequence of cDNA for mouse osteopontin-like protein.
A:Reference number: S04078; MUID:89263742; PMID:2726465
A:Accession: S04078
A:Molecule type: mRNA
A:Residues: 1-294 <MI2>
A:Cross-references: EMBL:X13986; NID:g53755; PIDN:CAA32165.1; PID:g53756
R:Yamamoto, S.
submitted to the EMBL Data Library, January 1990
A:Reference number: S12064
A:Accession: S12064
A:Molecule type: DNA
A:Residues: 1-121, 'P', 123-294 <YAM>
A:Cross-references: EMBL:X51834; NID:g53520; PIDN:CAA36132.1; PID:g297546
R:Craig, A.M.; Smith, J.H.; Denhardt, D.T.
J. Biol. Chem. 264, 9682-9689, 1989
A:Title: Osteopontin, a transformation-associated cell adhesion phosphoprotein, is indu
A:Reference number: A33853; MUID:89255479; PMID:2722855
A:Accession: A33853
A:Molecule type: mRNA
A:Residues: 1-98, 'G', 100-294 <CRA>
A:Cross-references: GB:J04806; NID:g200157; PIDN:AA57265.1; PID:g200158
R:Patarca, R.; Freeman, G.J.; Singh, R.P.; Wei, F.Y.; Duffee, T.; Blattner, F.; Regnier
J. Exp. Med. 170, 145-161, 1989
A:Title: Structural and functional studies of the early T lymphocyte activation 1 (Eta-
on.
A:Reference number: J0105; MUID:89310352; PMID:2787378
A:Accession: J0105
A:Molecule type: mRNA
A:Residues: 1-42, 'P', 44-294 <PAT>
A:Cross-references: EMBL:X16151; NID:g50863; PIDN:CAA34276.1; PID:g50864
R:Singh, R.P.; Patarca, R.; Schwartz, J.; Singh, P.; Cantor, H.
J. Exp. Med. 171, 1931-1942, 1990
A:Title: Definition of a specific interaction between the early T lymphocyte activation
A:Reference number: A60931; MUID:90278349; PMID:2351930
A:Accession: A60931
A:Molecule type: protein
A:Residues: 158-176 <SIN>
C:Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,
C:Genetics:
```

A:Gene: Eta-1
A:Map position: 5
A:Introns: 18/3; 30/3; 57/3; 71/3; 165/3
C:Superfamily: osteopontin
C:Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-294/Product: osteopontin #status predicted <MAT>
F:85-96/Region: aspartic acid-rich
F:144-146/Region: cell attachment (R-G-D) motif
F:78/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 1.7%; Score 7; DB 1; Length 294;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 THRLEHS 152
|||
DB 222 THRLEHS 228

RESULT 43
H70208
outer surface protein B precursor - Lyme disease spirochete plasmid A/lp54
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 04-Mar-2000
C:Accession: H70208
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, B.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: H70208
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-296 <KLE>
A:Cross-references: GB:AE000790; NID:G2690224; PIDN:AA066243.1; PID:G2690242; TIGR:BBA16
A:Experimental source: strain B31
C:Genetics:
A:Genome: plasmid
C:Superfamily: outer surface protein A
C:Keywords: blocked amino end; lipoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-296/Product: outer surface protein B #status predicted <MAT>
F:16/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
F:16/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
|||
DB 212 LKREIEK 218

RESULT 44
S06915
outer surface protein B precursor - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
C:Accession: S06915; I40262
R:Bergstrom, S.; Bundoc, V.G.; Barbour, A.G. Mol. Microbiol. 3, 479-486, 1989
A:Title: Molecular analysis of linear plasmid-encoded major surface proteins, OspA and C
A:Reference number: S06914; MUID:89343634; PMID:2761388
A:Accession: S06915
A:Molecule type: DNA
A:Residues: 1-296 <NER>
A:Cross-references: EMBL:X14407; NID:G393983; PIDN:CAA32580.1; PID:G393985
A:Experimental source: strain B31
R:Caporale, D.A.; Kocher, T.D.

Mol. Biol. Evol. 11, 51-64, 1994
A:Title: Sequence variation in the outer-surface-protein genes of Borrelia burgdorferi.
A:Reference number: I40249; MUID:94166630; PMID:8121286
A:Accession: I40262
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-296 <RES>
A:Cross-references: GB:L23142; NID:G349657; PIDN:AAA20956.1; PID:G349659
A:Experimental source: strain B31
C:Genetics:
A:Gene: ospB
C:Superfamily: outer surface protein A
C:Keywords: blocked amino end; lipoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-296/Product: outer surface protein A #status predicted <MAT>
F:16/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
F:16/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
|||
DB 212 LKREIEK 218

RESULT 45
I40260
outer surface protein B precursor - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 04-Mar-2000
C:Accession: I40260
R:Caporale, D.A.; Kocher, T.D. Mol. Biol. Evol. 11, 51-64, 1994
A:Title: Sequence variation in the outer-surface-protein genes of Borrelia burgdorferi.
A:Reference number: I40249; MUID:94166630; PMID:8121286
A:Accession: I40260
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-296 <RES>
A:Cross-references: GB:L23141; NID:G349654; PIDN:AAA20954.1; PID:G349656
C:Genetics:
A:Gene: OspB
C:Superfamily: outer surface protein A
C:Keywords: blocked amino end; lipoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-296/Product: outer surface protein B #status predicted <MAT>
F:16/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
F:16/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
|||
DB 212 LKREIEK 218

RESULT 46
I40258
outer surface protein B precursor - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 04-Mar-2000
C:Accession: I40258
R:Caporale, D.A.; Kocher, T.D. Mol. Biol. Evol. 11, 51-64, 1994
A:Title: Sequence variation in the outer-surface-protein genes of Borrelia burgdorferi.
A:Reference number: I40249; MUID:94166630; PMID:8121286
A:Accession: I40258
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A;Residues: 1-296 <RES>
A;Cross-references: GB:L23140; NID:G349651; PIDN:AAA20952.1; PID:G349653
C;Genetics:
A;Gene: ospB
C;Superfamily: outer surface protein A
C;Keywords: blocked amino end; lipoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-296/Product: outer surface protein B #status predicted <MAT>
F;16/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
F;16/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256
Db 212 LKREIEK 218

RESULT 47
140252
outer surface protein B precursor - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 04-Mar-2000
C;Accession: I40252
R;Caporale, D.A.; Kocher, T.D.
Mol. Biol. Evol. 11, 51-64, 1994
A;Title: Sequence variation in the outer-surface-protein genes of Borrelia burgdorferi.
A;Reference number: I40249; MUID:94166630; PMID:8121286
A;Accession: I40252
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-296 <RES>
A;Cross-references: GB:L23137; NID:G349642; PIDN:AAA22954.1; PID:G349644
A;Experimental source: strain 27985CT2
A;Accession: I40254
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-296 <RE2>
A;Cross-references: GB:L23138; NID:G349645; PIDN:AAA20948.1; PID:G349647
A;Experimental source: strain 1953SNY2
C;Genetics:
A;Gene: ospB
C;Superfamily: outer surface protein A
C;Keywords: blocked amino end; lipoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-296/Product: outer surface protein B #status predicted <MAT>
F;16/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
F;16/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256
Db 212 LKREIEK 218

RESULT 48
140264
outer surface protein B precursor - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 04-Mar-2000
C;Accession: I40264
R;Caporale, D.A.; Kocher, T.D.
Mol. Biol. Evol. 11, 51-64, 1994
A;Title: Sequence variation in the outer-surface-protein genes of Borrelia burgdorferi.
A;Reference number: I40249; MUID:94166630; PMID:8121286
A;Accession: I40264
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

A;Residues: 1-296 <RES>
A;Cross-references: GB:L23143; NID:G349660; PIDN:AAA20958.1; PID:G349662
C;Genetics:
A;Gene: ospB
C;Superfamily: outer surface protein A
C;Keywords: blocked amino end; lipoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-296/Product: outer surface protein B #status predicted <MAT>
F;16/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
F;16/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256
Db 212 LKREIEK 218

RESULT 49
140250
outer surface protein B precursor - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 04-Mar-2000
C;Accession: I40250
R;Caporale, D.A.; Kocher, T.D.
Mol. Biol. Evol. 11, 51-64, 1994
A;Title: Sequence variation in the outer-surface-protein genes of Borrelia burgdorferi.
A;Reference number: I40249; MUID:94166630; PMID:8121286
A;Accession: I40250
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-296 <RES>
A;Cross-references: GB:L23136; NID:G349639; PIDN:AAA22952.1; PID:G349641
C;Genetics:
A;Gene: ospB
C;Superfamily: outer surface protein A
C;Keywords: blocked amino end; lipoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-296/Product: outer surface protein B #status predicted <MAT>
F;16/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
F;16/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256
Db 212 LKREIEK 218

RESULT 50
140256
outer surface protein B precursor - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 04-Mar-2000
C;Accession: I40256
R;Caporale, D.A.; Kocher, T.D.
Mol. Biol. Evol. 11, 51-64, 1994
A;Title: Sequence variation in the outer-surface-protein genes of Borrelia burgdorferi.
A;Reference number: I40249; MUID:94166630; PMID:8121286
A;Accession: I40256
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-296 <RES>
A;Cross-references: GB:L23139; NID:G349648; PIDN:AAA20950.1; PID:G349650
C;Genetics:
A;Gene: ospB
C;Superfamily: outer surface protein A
C;Keywords: blocked amino end; lipoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>

F:16-296/Product: outer surface protein B #status predicted <MAT>
 F:16/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
 F:16/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LKREIEK 256
 |||||
 DB 212 LKREIEK 218

RESULT 51
 G84345
 hypothetical protein Vng1948h [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84345
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: R84160; MUID:20504483; PMID:11016950
 A:Accession: G84345
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-304 <STO>
 A:Cross-references: GB:AE004437; NID:gi0581386; PIDN:AAG20131.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VNG1948H

Query Match 1.7%; Score 7; DB 2; Length 304;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 EOLGYKT 181
 |||||
 DB 298 EOLGYKT 304

RESULT 52
 F90487
 maltose ABC transporter, permease SSO3058 [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
 C:Accession: F90487
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
 arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: F90487
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-322 <KUR>
 A:Cross-references: GB:AE006641; NID:gi13816462; PIDN:AAK43157.1; GSPDB:GN00155
 C:Genetics:
 A:Gene: SSO3058

Query Match 1.7%; Score 7; DB 2; Length 322;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LSGFVLG 16
 |||||
 DB 199 LSGFVLG 205

RESULT 53
 G84115
 ribose operon transcription repressor rbsR [imported] - Bacillus halodurans (strain C-1
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: G84115
 R:Takami, H.; Rakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: G84115
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-331 <STO>
 A:Cross-references: GB:AP001519; GB:BA000004; NID:gi0176109; PIDN:BAB07446.1; GSPDB:GNO
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: rbsR
 C:Superfamily: lac repressor

Query Match 1.7%; Score 7; DB 2; Length 331;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEEIEK 396
 |||||
 DB 97 TDEEIEK 103

RESULT 54
 T12728
 structural protein - Methanobacterium phage psiM2
 N:Alternate names: protein 12
 C:Species: Methanobacterium phage psiM2
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 04-Mar-2000
 C:Accession: T12728
 R:Frister, P.; Wasserfallen, A.; Stettler, R.; Leisinger, T.
 submitted to the EMBL Data Library, May 1998
 A:Description: Archaeophage PsiM2 complete genomic DNA.
 A:Reference number: Z17578
 A:Accession: T12728
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-351 <PFI>
 A:Cross-references: EMBL:AF065411; NID:g3249585; PID:g3249597; PIDN:AAC27051.1
 A:Experimental source: host Methanobacterium thermoautotrophicum strain Marburg
 C:Superfamily: Methanobacterium phage psiM2 structural protein

Query Match 1.7%; Score 7; DB 2; Length 351;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 EEDGSILK 210
 |||||
 DB 306 EEDGSILK 312

RESULT 55
 T17751
 hypothetical protein A257L - Chlorella virus PBCV-1
 C:Species: Chlorella virus PBCV-1
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T17751
 R:Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A:Reference number: Z18806
 A:Accession: T17751
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-361 <GRA>
 A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96625.1
 A:Experimental source: specific host Chlorella strain NC64A
 C:Genetics:
 A:Note: A257L

C:Superfamily: Chlorella virus PBCV-1 hypothetical protein A257L

Query Match 1.7%; Score 7; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 25 TDSDFEG 31
|||||
Db 260 TDSDFEG 266

RESULT 56
JC4748
polygalacturonase (EC 3.2.1.15) precursor - anthracnose fungus (Colletotrichum lindemuthianum)
N:Alternate names: pectin depolymerase; pectinase
C:Species: Colletotrichum lindemuthianum
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000
C:Accession: JC4748
R:Centis, S.; Dumas, B.; Fournier, J.; Marolda, M.; Esquerre-Tugaye, M.
Gene 170, 125-129, 1996
A:Title: Isolation and sequence analysis of Clpg1, a gene coding for an endopolygalacturonase
A:Reference number: JC4748; MUID:96200868; PMID:8621072
A:Accession: JC4748
A:Molecule type: DNA
A:Residues: 1-363 <CEN>
A:Cross-references: EMBL:X89370; NID:gl332456; PIDN:CAA61552.1; PID:gl332457
C:Comment: This enzyme catalyzes the hydrolytic cleavage of glycosidic alpha-1,4-linkage
C:Genetics:
A:Gene: Clpg1
A:Introns: 74/3
C:Superfamily: polygalacturonase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-363/Product: polygalacturonase #status predicted <MAT>
F:294/Active site: Asn #status predicted

Query Match 1.7%; Score 7; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 FVLGALA 19
|||||
Db 6 FVLGALA 12

RESULT 57
T32526
hypothetical protein CD4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32526
R:Du, Z.; Scheet, P.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid CD4.
A:Reference number: Z21185
A:Accession: T32526
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-378 <DUZ>
A:Cross-references: EMBL:AF036694; PIDN:AA88343.1; GSPDB:GN00022; CESP:CD4.5
A:Experimental source: strain Bristol N2; clone CD4
C:Genetics:
A:Gene: CESP:CD4.5
A:Map position: 4
A:Introns: 24/3; 108/3; 168/3; 214/2; 242/1; 288/3; 324/3; 352/1; 369/1

Query Match 1.7%; Score 7; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 201 KFFEEDG 207
|||||
Db 147 KFFEEDG 153

RESULT 58
T11892
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - sea anemone (Metridium senile)
C:Species: Metridium senile (brown sea anemone, frilled sea anemone)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T11892
R:Beagley, C.T.; Okimoto, R.; Wolstenholme, D.R.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z17371
A:Accession: T11892
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-385 <BEA>
A:Cross-references: EMBL:AF000023; NID:g2920983; PID:AA04638.1
A:Experimental source: white color morph
C:Genetics:
A:Genome: mitochondrion
A:Note: ND2
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 1.7%; Score 7; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 FVLGALA 19
|||||
Db 66 FVLGALA 72

RESULT 59
A86227
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A86227
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Conway, A.R.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86227
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-385 <STO>
A:Cross-references: GB:AE005172; NID:g3482913; PIDN:AAC33198.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 1.7%; Score 7; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 91 NVKQNVV 97
|||||
Db 47 NVKQNVV 53

RESULT 60
F70231
conserved hypothetical protein BGG06 - Lyme disease spirochete plasmid G/lp28-2
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: F70231
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit

son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, J.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 350, 580-586, 1997
A:Authors: Smith, H.C.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A:Reference number: AY0100; MUID:98065943; PMID:9403685

C:Accession: F70231

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-386 <KLE>

A:Cross-references: GB:AB000786; NID:g2690008; PIDN:AAC66054.1; PID:g2690011; TIGR:BBG06

A:Experimental source: strain B31

C:Genetics:

A:Genome: Plasmid

C:Superfamily: Lyme disease spirochaete plasmid conserved hypothetical protein BBG06

Query Match 1.7%; Score 7; DB 2; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LKKILSN 91

Db 248 LKKILSN 254

RESULT 61

T06997

probable glucose-6-phosphate/phosphate-translocator precursor - potato (fragment)

C:Species: Solanum tuberosum (potato)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 26-May-2000

C:Accession: T06997

R:Kammerer, B.; Fischer, K.; Hilpert, B.; Schubert, S.; Gutensohn, M.; Weber, A.; Flugge

Plant Cell 10, 105-117, 1998

A:Title: Molecular characterization of a carbon transporter in plastids from heterotroph

A:Reference number: Z14280; MUID:98138061; PMID:9477574

A:Accession: T06997

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-393 <KAM>

A:Cross-references: EMBL:AF020816; NID:g2997592; PIDN:AAC08526.1; PID:g2997593

A:Experimental source: plastid inner envelope membrane

C:Genetics:

A:Gene: GPT

A:Genome: nuclear

C:Function:

A:Description: mediates the antipport of glucose-6-phosphate against phosphate in plastid

C:Superfamily: triose phosphate/3-phosphoglycerate/phosphate translocator

C:Keywords: chloroplast; sugar transport

F;1-73/Domain: transit peptide (chloroplast) #status predicted <TNP>

F;74-393/Product: glucose-6-phosphate/phosphate-translocator #status predicted <MAT>

Query Match 1.7%; Score 7; DB 2; Length 393;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SAVLSGF 13

Db 48 SAVLSGF 54

RESULT 62

JQ0113

2-keto-3-deoxygluconate permease - *Erwinia chrysanthemi*

C:Species: *Erwinia chrysanthemi*

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999

C:Accession: JQ0113

R:Allen, C.; Reverchon, S.; Robert-Baudouy, J.

Gene 83, 233-241, 1989

A:Title: Nucleotide sequence of the *Erwinia chrysanthemi* gene encoding 2-keto-3-deoxyglu

A:Reference number: JQ0113; MUID:90060835; PMID:2684787

A:Accession: JQ0113

A:Molecule type: DNA

A:Residues: 1-398 <ALL>

A:Cross-references: GB:M31456; NID:gl148421; PIDN:AAA83925.1; PID:gl148422
C:Comment: *Erwinia chrysanthemi* is a phytopathogenic bacterium that incites soft rot di

C:Genetics:

A:Gene: kdgT

Query Match 1.7%; Score 7; DB 2; Length 398;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 FGRAVOT 197

Db 254 FGRAVOT 260

RESULT 63

C71538

hypothetical protein C71538 - *Chlamydia trachomatis* (serotype D, strain UW3/Cx)

C:Species: *Chlamydia trachomatis*

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: C71538

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia tra*

A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: C71538

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-404 <ARN>

A:Cross-references: GB:AE001298; GB:AE001273; NID:g3328659; PIDN:AAC67850.1; PID:g33286

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: C71538

Query Match 1.7%; Score 7; DB 2; Length 404;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 VKKNVVG 98

Db 239 VKKNVVG 245

RESULT 64

AH0051

probable O-antigen biosynthesis protein YPO0417 [imported] - *Yersinia pestis* (strain CO

C:Species: *Yersinia pestis*

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: AH0051

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AH0051

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-410 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89275.1; PID:gl5978513; GSPDB:GN00175

C:Genetics:

A:Gene: YPO0417

Query Match 1.7%; Score 7; DB 2; Length 410;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VLGAALF 20

Db 231 VLGAALF 237

RESULT 65

G70439

A; title: the complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A; accession number: A70300; MIM:198196666; PMID:9537320
A; accession: G70439
A; status: preliminary; nucleic acid sequence not shown; translation not shown
A; molecule type: DNA
A; residues: 1-413 <RF>
A; cross-references: GB:AE000748; NID:G2983960; PIDN:AAC07516.1; PID:G2983969; GB:AE00068
A; experimental source: strain VF5
C; Genetics:
A; Gene: aq 1618

G82777
glucamate symport protein XF0656 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequences_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: G82777
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleot
Nature 406, 151-157, 2000

A;Reference number: A09J17; MD5:806c2e277; refseq:AAAF83466.1; G
A;Note: for a complete list of authors see reference number A59328 below

A;Accession: G82777
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-437 <SIM>
A;Cross-references: GB:AEO03910; GB:AEO03849; NID:G9105532; PIDN:AAAF83466.1; G
A;Experimental source: strain 955C

2; Gene: XP0656
 C; Superfamily: Bacillus subtilis sodium-glutamate symporter homolog yncL
 Query Match 1.7%; Score 7; DB 2; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 19 GFVLGAL 25

RESULT 69
T21042
hypothetical protein F17A2.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

A;Residues: 1-463 <WII>
A;Cross-references: EMBL:Z68114; PIDN:CAA92158.1; GSPDB:GNO0028; CBSP:F17A2.3
A;Experimental source: Clone F17A2
C;Genetics:
A;Gene: CBSP:F17A2.3
A;Map position: X
A;Introns: 34/3; 148/3; 183/2; 212/1; 436/1

Query Match 1.7%; Score 7; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 IPEASPA 338
|||||
Db 347 IPEASPA 353

RESULT 70
A86465
Hypothetical protein F12G12.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: A86465
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86465
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-471 <STO>
A;Cross-references: GB:AB005172; NID:gl0086467; PIDN:AA012527.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 1.7%; Score 7; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 LLLTFSI 139
|||||
Db 194 LLLTFSI 200

RESULT 71
A56824
dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Haloferax volcanii
C;Species: Haloferax volcanii
C;Date: 18-Aug-1995 #sequence_revision 10-May-1996 #text_change 11-Jun-1999
C;Accession: A56824
R;Vettakkorumakav, N.N.; Stevenson, K.J.
Biochem. Cell Biol. 70, 656-663, 1992
A;Title: Dihydrolipoamide dehydrogenase from Haloferax volcanii: gene cloning, complete
A;Reference number: A56824; MUID:93119588; PMID:1339281
A;Accession: A56824
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 <VET>
A;Cross-references: GB:I09733; NID:gl43019; PIDN:AA072340.1; PID:gl49020
A;Note: sequence extracted from NCBI backbone (NCBI:122030, NCBI:P:122031)
C;Complex: dimer of identical chains containing a noncovalently bound FAD and a redox-ac
onents are pyruvate dehydrogenase and dihydrolipoamide acetyltransferase) and oxoglutar
ase)
C;Function:
A;Description: catalyzes the oxidation dihydrolipoamide to lipoamide using NAD acceptor;
nd pyruvate with the formation of succinyl-CoA and acetyl-CoA, respectively

C;Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
C;Keywords: FAD; flavoprotein; lipoamide; NAD; oxidoreductase; redox-active disulfide;
F;11-39/Region: beta-alpha-beta FAD nucleotide-binding fold
F;13-458/Domain: dihydrolipoamide dehydrogenase homology <BLD>
F;181-209/Region: beta-alpha-beta NAD nucleotide-binding fold
F;47-52/Disulfide bonds: redox-active #status predicted

Query Match 1.7%; Score 7; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SGFVLGA 17
|||||
Db 411 SGFVLGA 417

RESULT 72
T47480
Hypothetical protein F18N11.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47480
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unsel, M.; Mewes, H.W.; Lemcke, K
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
A;Accession: T47480
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 <JOR>
A;Cross-references: EMBL:AL132953
A;Experimental source: cultivar Columbia; BAC clone F18N11
C;Genetics:
A;Map position: 3
A;Introns: 290/3
A;Note: F18N11.160

Query Match 1.7%; Score 7; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 DIQKYP 66
|||||
Db 112 DIQKYP 118

RESULT 73
S51669
GCD10 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2422; protein YNL062c
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 21-Jul-1995 #text_change 23-Oct-1999
C;Accession: S51669; S58716; S62990
R;Garcia-Barrio, M.T.; Cuesta, R.; Hinnebusch, A.G.; Tamame Gonzalez, M.
submitted to the EMBL Data Library, December 1994
A;Reference number: S51669
A;Accession: S51669
A;Molecule type: DNA
A;Residues: 1-478 <GAR>
A;Cross-references: EMBL:X83511; NID:g603584; PIDN:CAA58501.1; PID:g603585
R;Bergsz, P.; Doignon, F.; Crouzet, M.
Yeast 11, 967-974, 1995
A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV
A;Reference number: S58711; MUID:96021608; PMID:8533472
A;Accession: S58716
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 132-478 <BER>
A;Cross-references: EMBL:U12141
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R;Bergsz, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62975
A;Accession: S62990

Query Match 1.7%; Score 7; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 DIQKYP 66
|||||
Db 112 DIQKYP 118

RESULT 73
S51669
GCD10 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2422; protein YNL062c
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 21-Jul-1995 #text_change 23-Oct-1999
C;Accession: S51669; S58716; S62990
R;Garcia-Barrio, M.T.; Cuesta, R.; Hinnebusch, A.G.; Tamame Gonzalez, M.
submitted to the EMBL Data Library, December 1994
A;Reference number: S51669
A;Accession: S51669
A;Molecule type: DNA
A;Residues: 1-478 <GAR>
A;Cross-references: EMBL:X83511; NID:g603584; PIDN:CAA58501.1; PID:g603585
R;Bergsz, P.; Doignon, F.; Crouzet, M.
Yeast 11, 967-974, 1995
A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV
A;Reference number: S58711; MUID:96021608; PMID:8533472
A;Accession: S58716
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 132-478 <BER>
A;Cross-references: EMBL:U12141
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R;Bergsz, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62975
A;Accession: S62990

A:Molecule type: DNA
A:Residues: 1-478 <BEW>
A:Cross-references: EMBL:Z71338; NID:gl301936; PIDN:CAA95935.1; PID:e239899; PID:gl30193
A:Experimental source: strain G288C
C:Genetics:
A:Gene: SGD:GDC10
A:Cross-references: SGD:S0005006; MIPS:YNL062c
A:Map position: 14L

Query Match 1.7%; Score 7; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EEIEKWK 398
DB 142 EEIEKWK 148

RESULT 74
F81220
NADH dehydrogenase I, N chain NMB0259 [imported] - Neisseria meningitidis (strain MC58 s
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: F81220
R:Petzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81220
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-480 <TET>
A:Cross-references: GB:AE002382; GB:AE002098; NID:g7225470; PIDN:AAF40713.1; PID:g722548
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0259
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2

Query Match 1.7%; Score 7; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
DB 163 FVLGALA 169

RESULT 75
G81796
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain N NMA2228 [imported] - Neisseria men
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 03-Jun-2002
C:Accession: G81796
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: G81796
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <PAR>
A:Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85439.1; PID:g738084
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: nuoN; NMA2228
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C:Keywords: NAD; oxidoreductase

Query Match 1.7%; Score 7; DB 2; Length 481;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
DB 163 FVLGALA 169

RESULT 76
F71210
hypothetical protein PH1950 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: F71210
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: F71210
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-483 <KAW>
A:Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA31077.1; PID:g3258394
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1950
C:Superfamily: Thermotoga maritima hypothetical protein MTH1256

Query Match 1.7%; Score 7; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DLVFLLL 135
DB 255 DLVFLLL 261

RESULT 77
F89933
hypothetical protein SA1365 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Dec-2002
C:Accession: F89933
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701333; PIDN:BA842627.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1365
C:Superfamily: glycine dehydrogenase (decarboxylating)

Query Match 1.7%; Score 7; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLOEELK 227
DB 119 SLOEELK 125

RESULT 78
A28582
tyrosine 3-monooxygenase (EC 1.14.16.2) - quail

N/Alternate names: tyrosine 3-hydroxylase
C/Species: Phasianidae Gen. sp. (quail)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 31-Mar-2000
C/Accession: A28582; PH1524
R/Fauquet, M.; Grima, B.; Lanouroux, A.; Mallet, J.
J. Neurochem. 50, 142-148, 1988
A/Title: Cloning of quail tyrosine hydroxylase: amino acid homology with other hydroxylase
A/Reference number: A28582; MUID:88089590; PMID:2447231
A/Accession: A28582
A/Molecule type: mRNA
A/Residues: 1-491 <FAU>
A/Cross-references: GB:M24778; NID:G213649; PIDN:AAA49514.1; PID:G213650
R/Fauquet, M.; Boni, C.
J. Neurochem. 60, 274-281, 1993
A/Title: The quail tyrosine hydroxylase gene promoter contains an active cyclic AMP-resp
A/Reference number: PH1524; MUID:93107923; PMID:8093261
A/Accession: PH1524
A/Molecule type: DNA
A/Residues: 1-30 <FA2>
C/Superfamily: phenylalanine 4-monooxygenase
C/Keywords: biotin; catecholamine biosynthesis; iron; metalloprotein; oxidoreductase;
F:324,329,369/Binding site: iron (His, His, Glu) #status predicted

Query Match 1.7%; Score 7; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 TDEIEK 396
DB 353 TDEIEK 359

RESULT 79
T16417
Hypothetical protein F52C9.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000
C/Accession: T16417
R/Favella, T.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid F52C9.
A/Reference number: Z18511
A/Accession: T16417
A/Molecule type: DNA
A/Residues: 1-498 <PAV>
A/Cross-references: EMBL:U39850; NID:G1055052; PID:G1055053; PIDN:AAA81055.1; CESP:F52C9
C/Genetics:
A/Gene: CESP:F52C9.5
A/Introns: 45/2; 87/3; 132/1; 185/3; 207/1; 294/3; 337/1; 381/3; 430/1
C/Superfamily: Caenorhabditis elegans hypothetical protein F52C9.5

Query Match 1.7%; Score 7; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.4e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 FKSRLL 363
DB 491 FKSRLL 497

RESULT 80
D82081
UDP-N-acetylmuramate-alanine ligase VC2400 [imported] - Vibrio cholerae (strain N16961)
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: D82081
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301

A/Accession: D82081
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-506 <HEI>
A/Cross-references: GB:AE003852; NID:G9656963; PIDN:AAF95543.1; GSPDB:GN00
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC2400
A/Map position: 1
C/Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 1.7%; Score 7; DB 2; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 IQAREK 268
DB 118 IQAREK 124

RESULT 81
T01870
Probable pectinesterase (EC 3.1.1.11) - Arabidopsis thaliana
N/Alternate names: protein T24M8.6
C/Species: Arabidopsis thaliana (mouse-ear cross)
C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 26-Aug-1999
C/Accession: T01870
R/Latrelle, P.; Elliott, G.; Le, T.
submitted to the EMBL Data Library, August 1998
A/Description: The sequence of A. thaliana T24M8.
A/Reference number: Z14449
A/Accession: T01870
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-536 <LAT>
A/Cross-references: EMBL:AF077409; NID:G3319365; PID:G3319371
A/Experimental source: cultivar Columbia
C/Genetics:
A/Map position: 4
A/Introns: 208/3; 298/1
A/Note: T24M8.6
C/Superfamily: pectinesterase
C/Keywords: carboxylic ester hydrolase

Query Match 1.7%; Score 7; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 EQALKKI 88
DB 208 EQALKKI 214

RESULT 82
T44683
Precorrin methylase (EC 2.1.1.-) [imported] - Bacillus megaterium
C/Species: Bacillus megaterium
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C/Accession: T44683
R/Raux, E.; Lanois, A.; Warren, M.J.; Rambach, A.; Thermes, C.
Biochem. J. 335, 159-166, 1998
A/Title: Cobalamin (vitamin B12) biosynthesis: identification and characterization of a
A/Reference number: Z22829; MUID:98416126; PMID:9742225
A/Accession: T44683
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-540 <RAU>
A/Cross-references: EMBL:AJ000759; NID:G3724036; PIDN:CAA04307.1; PID:G3724038
A/Experimental source: strain DSM 509
C/Genetics:
A/Note: cbiH60
C/Keywords: methyltransferase

Query Match 1.7%; Score 7; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GESTSAV 9
|||
Db 313 GESTSAV 319
|||

RESULT 83
F72268
ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: F72268
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; PMID:99287316; PMID:10360571
A/Accession: F72268
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-564 <ARN>
A/Cross-references: GB:AE001786; GB:AE000512; NID:94981873; PIDN:AAD36392.1; PID:9498187
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TM1319
C/Suprafamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.7%; Score 7; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LVFLLLT 136
|||
Db 62 LVFLLLT 68
|||

RESULT 84
F82595
glutathione-regulated potassium efflux system protein XF2140 [imported] - Xylella fastid
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C/Accession: F82595
R/Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; PMID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: F82595
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-572 <SIM>
A/Cross-references: GB:AE004028; GB:AE003849; NID:9107266; PIDN:AAR84939.1; GSPDB:GN001
A/Experimental source: strain 94SC
R/Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
as-Neco, E.; Docena, C.; El-Dorry, H.; Facinani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XF2140

C/Suprafamily: glutathione-regulated potassium efflux system protein kefc
Query Match 1.7%; Score 7; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FVLGALA 19
|||
Db 19 FVLGALA 25
|||

RESULT 85
AC2395
ATP-binding protein of ABC transporter alr4715 [imported] - Nostoc sp. (strain PCC 7120
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C/Accession: AC2395
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A/Reference number: AB1807; PMID:21595285; PMID:11759840
A/Accession: AC2395
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-583 <KUR>
A/Cross-references: GB:BA000019; PIDN:BA876414.1; PID:gl7133852; GSPDB:GN00179
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr4715
C/Suprafamily: Escherichia coli ABC transporter mdla; ATP-binding cassette homology

Query Match 1.7%; Score 7; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LGEVKGE 40
|||
Db 333 LGEVKGE 339
|||

RESULT 86
AD2594
hypothetical protein cysJ [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: AD2594
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:21608550; PMID:11741193
A/Accession: AD2594
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-589 <KUR>
A/Cross-references: GB:AE008688; PIDN:AAL41170.1; PID:gl7738469; GSPDB:GN00186
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: cysJ
A/Map position: circular chromosome
C/Suprafamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferrihemoprotein x
C/Keywords: flavoprotein

Query Match 1.7%; Score 7; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 VNRLKRE 253
|||


```

Db      575 VNRLKRE 581
|||||
RESULT 87
E97376
C:Species: Agrobacterium tumefaciens (strain C59)
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: E97376
A:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: E97376
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-589 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK85966.1; PID:gl5155025; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C 238
A:Map position: circular chromosome
C:Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferrihemoprotein re
C:Keywords: flavoprotein

Query Match      1.7%; Score 7; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      247 VNRLKRE 253
|||||
Db      575 VNRLKRE 581
|||||
RESULT 88
S28036
C:Species: Streptococcus pneumoniae
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000
C:Accession: S28036
R:Martin, C.; Sibold, C.; Hakenbeck, R.
EMBO J. 11, 3831-3836, 1992
A>Title: Relatedness of penicillin-binding protein 1a genes from different clones of pen
A:Reference number: S28031; MUID:93010977; PMID:1396576
A:Accession: S28036
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-608 <MAR>
A:Cross-references: EMBL:X67871; NID:g47415; PIDN:CAA48071.1; PID:g47416
C:Superfamily: penicillin-binding protein 1B

Query Match      1.7%; Score 7; DB 2; Length 608;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      390 TDEIEK 396
|||||
Db      564 TDEIEK 570
|||||
RESULT 89
G70039
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: G70039
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
A:Title: conserved hypothetical protein yvgJ - Bacillus subtilis
A:Reference number: S28031; MUID:93010977; PMID:1396576
A:Accession: S28036
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-608 <MAR>
A:Cross-references: EMBL:X67871; NID:g47415; PIDN:CAA48071.1; PID:g47416
C:Superfamily: penicillin-binding protein 1B

Query Match      1.7%; Score 7; DB 2; Length 608;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      390 TDEIEK 396
|||||
Db      564 TDEIEK 570
|||||
RESULT 89
G70039
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: G70039
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
A:Title: conserved hypothetical protein yvgJ - Bacillus subtilis
A:Reference number: S28031; MUID:93010977; PMID:1396576
A:Accession: S28036
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-608 <MAR>
A:Cross-references: EMBL:X67871; NID:g47415; PIDN:CAA48071.1; PID:g47416
C:Superfamily: penicillin-binding protein 1B

Query Match      1.7%; Score 7; DB 2; Length 608;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      390 TDEIEK 396
|||||
Db      564 TDEIEK 570
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```

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: G70039
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-617 <KUN>
A:Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15341.1; PID:g2635849
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvgJ
C:Superfamily: Bacillus subtilis probable anion-binding protein yfE

Query Match      1.7%; Score 7; DB 2; Length 617;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      129 DLVFLLL 135
|||||
Db      128 DLVFLLL 134
|||||
RESULT 90
H69590
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: H69590
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
A:Title: conserved hypothetical protein yvgJ - Bacillus subtilis
A:Reference number: S28031; MUID:93010977; PMID:1396576
A:Accession: S28036
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-632 <KUN>
A:Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB15032.1; PID:g2635538
A:Experimental source: strain 168
C:Genetics:
A:Gene: asnB
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)

Query Match      1.7%; Score 7; DB 2; Length 632;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      24 NTDSDTE 30
|||||
Db      98 NTDSDTE 104
|||||
RESULT 91
D72605
A:Title: probable long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) APE1307 [similarity] - Aeropyrum

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C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 03-Jun-2002
C/Accession: D72605
R/Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kawa, S.; 6, 83-101, 1999
DNA Res. 5, 55-76, 1998
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: D72605
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-651 <KAW>
A/Cross-references: DDBJ:AP000061; NID:95104821; PIDN:BAA80298.1; PID:G5104984
A/Experimental source: strain K1
C/Genetics:
A/Gene: APE1307
C/Superfamily: Synchocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolog F/71-606/Domain: acetate-CoA ligase homolog <ACL>

Query Match 1.7%; Score 7; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LKREIEK 256
Db 561 LKREIEK 567

RESULT 92
E82954
conserved hypothetical protein PA5544 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: E82954
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: E82954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-674 <STO>
A/Cross-references: GB:AE004966; GB:AE004091; NID:99951872; PIDN:AAG08929.1; GSPDB:GN001
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA5544

Query Match 1.7%; Score 7; DB 2; Length 674;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GFVLGAL 18
Db 652 GFVLGAL 658

RESULT 93
E69135
coenzyme F420-reducing hydrogenase, beta subunit homolog - Methanobacterium thermoautotrophicum
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
C/Accession: E69135
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vicair, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional genome
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: E69135
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
A/Residues: 1-689 <WTH>
A/Cross-references: GB:AE000813; GB:AE000666; NID:92621320; PIDN:AAB84786.1; PID:G26213
A/Experimental source: strain Delta H
C/Genetics:
A/Gene: MTH280
C/Superfamily: unassigned ferredoxin 2[4Fe-4S]-related proteins; ferredoxin 2[4Fe-4S] h F/78-132/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 1.7%; Score 7; DB 2; Length 689;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 REIEKRR 258
Db 391 REIEKRR 397

RESULT 94
T18665
hypothetical protein B0035.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C/Accession: T18665
R/White, S.
Submitted to the EMBL Data Library, May 1996
A/Reference number: Z19002
A/Accession: T18665
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-727 <WIL>
A/Cross-references: EMBL:Z73102; PIDN:CAA97420.1; GSPDB:GN00022; CESP:B0035.6
A/Experimental source: clone B0035
C/Genetics:
A/Gene: CESP:B0035.6
A/Map position: 4
A/Introns: 28/3; 66/2; 156/3; 578/3; 640/1; 714/1
C/Superfamily: Caenorhabditis elegans hypothetical protein B0035.6

Query Match 1.7%; Score 7; DB 2; Length 727;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 LLTPSII 140
Db 314 LLTPSII 320

RESULT 95
B71009
hypothetical protein PH1368 - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
C/Accession: B71009
R/Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushi, N.; Oguchi, Y.; 5, 55-76, 1998
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic Pyrococcus horikoshii
A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: B71009
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-728 <KAW>
A/Cross-references: GB:AP000006; NID:G3236133; PIDN:BAA30474.1; PID:G3257791
A/Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Gene: PH1368
C/Superfamily: Pyrococcus abyssi hypothetical protein PA82446

Query Match 1.7%; Score 7; DB 2; Length 728;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 LLLTSP1 139
 |||||
 Db 12 LLLTSP1 18

RESULT 96

T05409
 hypothetical protein F10M6.170 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cross)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C/Accession: T05409
 R/Bevan, M.; Weichselgartner, M.; Partmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; N
 submitted to the Protein Sequence Database, February 1998
 A/Reference number: Z15414
 A/Accession: T05409
 A/Molecule type: DNA
 A/Residues: 1-764 <BEV>
 A/Cross-references: EMBL:AL021811
 A/Experimental source: cultivar Columbia; BAC clone F10M6
 C/Genetics:
 A/Map position: 4
 A/Map: F10M6.170

Query Match 1.7%; Score 7; DB 2; Length 764;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 SLQSELK 227
 |||||
 Db 146 SLQSELK 152

RESULT 97

IS1083
 SOX-L2 - rainbow trout
 C/Species: Oncorhynchus mykiss (rainbow trout)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C/Accession: IS1083
 R/Takamatsu, N.; Kanda, H.; Tsuchiya, I.; Yamada, S.; Ito, M.; Kabeno, S.; Shiba, T.; Ya
 Mol. Cell. Biol. 15, 3759-3766, 1995
 A/Title: A gene that is related to SRV and is expressed in the testes encodes a leucine
 A/Reference number: IS1083; MUID:95311974; PMID:7791783
 A/Accession: IS1083
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-767 <YAK>
 A/Cross-references: GB:D61688; NID:927216; PIDN:BAA09617.1; PID:g927217
 C/Superfamily: HMG box homology
 F:554-629/Domain: HMG box homology <HMG1>

Query Match 1.7%; Score 7; DB 2; Length 767;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LLGEVKG 39
 |||||
 Db 173 LLGEVKG 179

RESULT 98

T27941
 hypothetical protein ZK562.3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C/Accession: T27941
 R/White, S.
 submitted to the EMBL Data Library, August 1996
 A/Reference number: Z20444
 A/Accession: T27941
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-780 <WIL>

A/Cross-references: EMBL:Z79604; PIDN:CAB01900.1; GSPDB:GN00028; CESP:ZK662.3
 A/Experimental source: clone ZK662
 C/Genetics:
 A/Gene: CESP:ZK662.3
 A/Map position: X
 A/Introns: 30/1; 56/1; 98/3; 176/3; 206/3; 289/2; 311/1; 341/3; 444/3; 507/3; 655/1; 68

Query Match 1.7%; Score 7; DB 2; Length 780;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 DEIERM 397
 |||||
 Db 593 DEIERM 599

RESULT 99

S51592
 XynB precursor - Ruminococcus flavefaciens
 C/Species: Ruminococcus flavefaciens
 C/Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 15-Oct-1999
 C/Accession: S51592
 R/Zhang, J.X.; Martin, J.; Flint, H.J.
 Mol. Gen. Genet. 245, 260-264, 1994
 A/Title: Identification of non-catalytic conserved regions in xylanases encoded by the
 A/Reference number: S51592; MUID:95115675; PMID:7816035
 A/Accession: S51592
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-781 <ZHA>

A/Cross-references: EMBL:Z35226; NID:9516273; PIDN:CAA84537.1; PID:G516274
 C/Superfamily: endo-1,4-beta-xylanase homology; Thermotoga xylanase A amino-terminal re
 F:42-239/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:258-401/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA>

Query Match 1.7%; Score 7; DB 2; Length 781;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 ALXKILS 90
 |||||
 Db 5 ALXKILS 11

RESULT 100

G95112
 exoribonuclease, VacB/Rnb family [imported] - Streptococcus pneumoniae (strain TIGR4)
 C/Species: Streptococcus pneumoniae
 C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
 C/Accession: G95112
 R/Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 Science 293, 498-506, 2001
 A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
 A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A/Reference number: A95000; MUID:21357209; PMID:11463916
 A/Accession: G95112
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-784 <KUR>
 A/Cross-references: GB:AE005672; PIDN:AAK75096.1; PID:gl4972450; GSPDB:GN00164; TIGR:SP
 A/Experimental source: strain TIGR4
 C/Genetics:
 A/Gene: SP0975
 C/Superfamily: virulence-associated protein vacB homolog

Query Match 1.7%; Score 7; DB 2; Length 784;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 FEEDGSL 209
 |||||

Db 50 FEEDSL 56

Search completed: April 16, 2004, 10:20:59
Job time : 35 secs